

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 06-22-04
Searcher: Beverly C 2528
Terminal time: 20
Elapsed time: _____
CPU time: _____
Total time: 23
Number of Searches: _____
Number of Databases: 1

Search Site

____ STIC
____ CM-1
____ Pre-S

Type of Search

____ N.A. Sequence
____ A.A. Sequence
____ Structure
____ Bibliographic

Vendors

____ IG
____ STN
____ Dialog
____ APS
____ Geninfo
____ SDC
____ DARC/Questel
____ Other CGW

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2004, 09:36:12 ; Search time 14423 Seconds
(without alignments)
17495.885 Million cell updates/sec

Title: US-09-924-197-1
Perfect score: 5822
Sequence: 1 cttgcacgacaggtttccg.....tgccgattcattatgcag 5822

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
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- 14: gb.vi.*
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- 16: em.fun.*
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- 18: em.in.*
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- 38: em.sy.*
- 39: em.hgo.hum.*
- 40: em.hgo.mus.*
- 41: em.hgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2892	49.7	4486	12	EVCOR116N	Z29589 Expression
2	2760.8	47.4	4412	12	EVCOR112N	Z29587 Expression
3	2755.6	47.3	5534	6	AR037157	AR037157 Sequence
4	2755.6	47.3	5534	6	AR112043	AR112043 Sequence
5	2705.8	46.5	4350	12	AF173954	AF173954 Cloning v
6	2705.8	46.5	5558	12	AF173955	AF173955 Cloning v
7	2686	46.1	4229	6	E63777	E63777 Method for
8	2683.4	46.1	3448	6	AX590988	AX590988 Sequence
9	2683.4	46.1	3448	6	AX591141	AX591141 Sequence
10	2683.4	46.1	3448	6	AX717564	AX717564 Sequence
11	2683.4	46.1	3551	12	AY122058	AY122058 Expressio
12	2677	46.0	3711	12	AF525778	AF525778 Expressio
13	2677	46.0	3033	12	CVGEM7LICF	U25272 Ligation-in
14	2677	46.0	3033	12	CVGEM7LICR	U25268 Ligation-in
15	2677	46.0	7823	12	AF041426	AF041426 Cloning v
16	2677	46.0	8658	12	AF338824	AF338824 Cloning v
17	2677	46.0	8696	12	AF379854	AF379854 Cloning v
18	2675.4	46.0	3018	6	A98767	A98767 Sequence 4
19	2671.6	45.9	3877	12	AB038599	AB038599 Cloning v
20	2671.6	45.9	6320	12	AB038600	AB038600 Cloning v
21	2668.6	45.8	4514	6	AX781452	AX781452 Sequence
22	2668.6	45.8	4514	6	AX816961	AX816961 Sequence
23	2658.4	45.7	9359	6	AX384394	AX384394 Sequence
24	2658.4	45.7	9359	6	AX473364	AX473364 Sequence
25	2654.6	45.6	2943	12	AF092940	AF092940 Cloning v
26	2654.6	45.6	3012	12	AF092546	AF092546 Cloning v
27	2641.4	45.4	2997	12	CVGEM72FP	X65310 Cloning vec
28	2641.4	45.4	3000	12	CVGEM52FP	X65308 Cloning vec
29	2641.4	45.4	3404	6	AX771236	AX771236 Sequence
30	2630.4	45.2	3485	6	AR199035	AR199035 Sequence
31	2553	43.9	6824	6	A25909	A25909 Synthetic Y
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33	2552	43.8	10450	12	AF218466	AF218466 Activatio
34	2551.8	43.8	37808	6	AX001082	AX001082 Sequence
35	2550	43.8	4883	6	AR220205	AR220205 Sequence
36	2550	43.8	4883	6	AX358365	AX358365 Sequence
37	2550	43.8	11038	12	AY196826	AY196826 Piggybac
38	2549	43.8	2958	6	AX247549	AX247549 Sequence
39	2549	43.8	2958	6	AX247550	AX247550 Sequence
40	2549	43.8	2958	6	AX247551	AX247551 Sequence
41	2549	43.8	2967	12	U02449	U02449 Cloning vec
42	2547.4	43.8	4133	12	U01668	U01668 Phagemid cl
43	2542.6	43.7	2959	12	AF118920	AF118920 Cloning v
44	2538.2	43.6	10597	6	AX006825	AX006825 Sequence
45	2538.2	43.6	10597	6	AX417673	AX417673 Sequence

ALIGNMENTS

RESULT 1
LOCUS EVCOR116N 4486 bp DNA linear SYN 24-MAR-1994
DEFINITION Expression vector pCOR116N (modified from pCOR116 in [3]).
ACCESSION Z29589.1 GI:452348
VERSION 1
KEYWORDS ampicillin resistance; beta-lactamase; colE1 origin; expression vector; nos terminator; phage fl region; rice actin1 promoter.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 49 to 304)
AUTHORS Depicker,A., Stachel,S., Dhaese,P., Zambryski,P. and Goodman,H.M.
TITLE Napaline synthase: transcript and DNA sequence
JOURNAL J. Gen. Appl. Microbiol. 1, 561-573 (1982)

REFERENCE 2
 AUTHORS McElroy, D., Blowers, A.D., Jenes, B. and Wu, R.
 TITLE Construction of expression vectors based on the rice actin 1 (Act1)
 JOURNAL Mol. Gen. Genet. 231 (1), 150-160 (1991)
 MEDLINE 92092956
 PUBMED 1753941
 REMARK (sites)
 3 (bases 1 to 4486)
 AUTHORS Liu, L., Dasgupta, I., Davies, J. and Hull, R.
 TITLE Modified expression vectors for monocot transformation toward virus resistance
 JOURNAL Unpublished
 AUTHORS Liu, L.
 TITLE Direct Submission
 JOURNAL Submitted (26-JAN-1994) Liu L., John Innes Institute, Virus Research, Colney Lane, Norwich, United Kingdom, NR4 7UH
 FEATURES Location/Qualifiers
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 Db 49 GCAGATCGTTCAACATTTGGCAATTAAGTTTCTTAAGATTGAATTCCTTTCGCGGTCTT 108
 QY 2897 GCAGATGATTATCATATAATTTCTGTTGAATTACGTTAAGCATTGAATTAATTAACATGTAA 2956
 Db 109 GCGATGATTATCATATAATTTCTGTTGAATTACGTTAAGCATTGAATTAATTAACATGTAA 168
 QY 2957 TCATGATCGTTATTTATCAGATGGGTTTTATGATTAGAGTCCCGCAATTATACATTTAA 3016
 Db 169 TGCATGATCGTTATTTATCAGATGGGTTTTATGATTAGAGTCCCGCAATTATACATTTAA 228
 QY 3017 TACGCGATAGAAACAAATATAGCGCGCAACTAGGATAAATTATCGCGCGGTGTCA 3076
 Db 229 TACGCGATAGAAACAAATATAGCGCGCAACTAGGATAAATTATCGCGCGGTGTCA 288

QY 3077 TCTATGTTACTAGATCGACCTGCGGCGATGGATCGGCGCGCATGCGATCGCGCGCC 3136
 Db 289 TCTATGTTACTAGAT-----CTTAGAGTCACGGGCC 322
 QY 3137 AATTGCGCCCTATAGTAGTCTGATTAACAATTCACTGGCGCGTCTGTTTAAACAGTCTGTAC 3196
 Db 323 AATTGCGCCCTATAGTAGTCTGATTAACAATTCACTGGCGCGTCTGTTTAAACAGTCTGTAC 382
 QY 3197 TGGGAAAACCTTGGCGTTTACCCAACTTAATCGCTTGCAGACATATCCCTTTGCCAGC 3256
 Db 383 TGGGAAAACCTTGGCGTTTACCCAACTTAATCGCTTGCAGACATATCCCTTTGCCAGC 442
 QY 3257 TGGCGTAATAGCGAAGAGCGCCGACCGATCGCCCTCCCAACAGTTGCGGAGCTGAAT 3316
 Db 443 TGGCGTAATAGCGAAGAGCGCCGACCGATCGCCCTCCCAACAGTTGCGGAGCTGAAT 502
 QY 3317 GCGAATGAGCGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGTGGTGTACGCGCA 3376
 Db 503 GCGAATGAGCGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGTGGTGTACGCGCA 562
 QY 3377 GCGTGACCGCTACATTTGCCAGCGCCCTAGCGCGCGCTCTTTTCGCTTTCTTCCTTCCT 3436
 Db 563 GCGTGACCGCTACATTTGCCAGCGCCCTAGCGCGCGCTCTTTTCGCTTTCTTCCTTCCT 622
 QY 3437 TTCTCGCCACGTTTCGCGCGCTTTCCCGTCAAGCTCTAAATCGGGGCTCCCTTTAGGT 3496
 Db 623 TTCTCGCCACGTTTCGCGCGCTTTCCCGTCAAGCTCTAAATCGGGGCTCCCTTTAGGT 682
 QY 3497 TCGGATTTAGAGCTTTACGGCACCTCGACCGCAAAACCTTGATTTGGGTGATGTTTAC 3556
 Db 683 TCGGATTTAGAGCTTTACGGCACCTCGACCGCAAAACCTTGATTTGGGTGATGTTTAC 742
 QY 3557 GTAGTGGCCATCGCCCTGATAGACGTTTTCGCCCTTTGAGCTTGGAGTCCACGTTCT 3616
 Db 743 GTAGTGGCCATCGCCCTGATAGACGTTTTCGCCCTTTGAGCTTGGAGTCCACGTTCT 802
 QY 3617 TTAATAGTGAATCTTGTTCMAAATCGGAACACACTCAACCTTCTCGCTCTATCTTCTT 3676
 Db 803 TTAATAGTGAATCTTGTTCMAAATCGGAACACACTCAACCTTCTCGCTCTATCTTCTT 862
 QY 3677 TTGATTTAAGGATTTTTCGCGATTTTCGCGATTTTCGCGATTTTAAAAATGAGCTGATTTAA 3736
 Db 863 TTGATTTAAGGATTTTTCGCGATTTTTCGCGATTTTAAAAATGAGCTGATTTAA 922
 QY 3737 AAATATTTAACCGAATTTTAAACAATTAACGTTTAAATTCGCGCTGATGCGGTAT 3796
 Db 923 AAATATTTAACCGAATTTTAAACAATTAACGTTTAAATTCGCGCTGATGCGGTAT 982
 QY 3797 TTTCTCTTACGATCTGTGCGGTATTTTCAACCGCATACAGTGGCAGCTTTTCGCGGAA 3856
 Db 983 TTTCTCTTACGATCTGTGCGGTATTTTCAACCGCATACAGTGGCAGCTTTTCGCGGAA 1042
 QY 3857 ATGTCGGGGAACCCCTATTTCTTATTTTCTAAATACATCAAAATATGATTCGCTCA 3916
 Db 1043 ATGTCGGGGAACCCCTATTTCTTATTTTCTAAATACATCAAAATATGATTCGCTCA 1102
 QY 3917 TGACACAATAACCCGATTAATGCTCAATATATTGAAGAAGAGATGATGATTTTC 3976
 Db 1103 TGACACAATAACCCGATTAATGCTCAATATATTGAAGAAGAGATGATGATTTTC 1162
 QY 3977 AACATTTCCGTGCGCCCTTATTCCTTTTTCGCGCATTTTTCGCTTCTGTTTTCGTC 4036
 Db 1163 AACATTTCCGTGCGCCCTTATTCCTTTTTCGCGCATTTTTCGCTTCTGTTTTCGTC 1222
 QY 4037 ACCCAGAACCCGTGTAAGTAAAGATGCTGAAGATGCTGAAGATGCTGAAGTGGTTC 4096
 Db 1223 ACCCAGAACCCGTGTAAGTAAAGATGCTGAAGATGCTGAAGTGGTTC 1282
 QY 4097 ACATCGAACTGGATCTCAACAGCGTAAAGTCCCTTGAAGTTCGCGCCGAGACGTT 4156
 Db 1283 ACATCGAACTGGATCTCAACAGCGTAAAGTCCCTTGAAGTTCGCGCCGAGACGTT 1342
 QY 4157 TTCCAATGATGAGCACTTTTAAAGTTCTGTATGTGGCGCGGTATTTATCCCGTATTGACG 4216

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QY	4217	CGGGCAAGCAACTCGGTGCGCGCATACACTATTCTCAGATGACTTGGTTGAGTACT	4276	5297	AGCGCAGCGGTGCGCTGAACGGGGGTTCTGTGCACACAGACCCAGCTTGGAGCGAACGA	5356
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QY	4277	CACCACTCAGAAAAAGCATTTTACGATGGCATGACAGTAAGAGAAATTATGACAGTCTG	4336	5357	CCTACACCCAACTGAGATACCTACAGCGTGAAGTATGAGAAAGCGCCAGCTTCCCGAAG	5416
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QY	4337	CCATAACCATGAGTATACACTCGCGCCAACTTCTCTGACAAAGCATCGGAGGACCGA	4396	5417	GGAGAAAGCGGACAGGTATCCGTTAAGCGGCGAGGTGCGAACAGGAGCGCACGAGGG	5476
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QY	4397	AGGAGCTAACCGCTTTTTCACAAATGCGGGCATCATGTAACTCGCGCTTGTATCGTTGGG	4456	5477	AGCTTCCAGGGGGAACGCTGTATCTTTATAGTCTCTGTGCGGTTTTCGCCACCTCTGAC	5536
Db	1583	AGGAGCTAACCGCTTTTTCACAAATGCGGGCATCATGTAACTCGCGCTTGTATCGTTGGG	1642	2663	AGCTTCCAGGGGGAACGCTGTATCTTTATAGTCTCTGTGCGGTTTTCGCCACCTCTGAC	2722
QY	4457	AACCGGAGCTGAATGAAGCCATACCAAAACGAGCGGTGACACACGATGCTGTAGCAA	4516	5537	TTGAGCGTTCGATTTTGTGATGCTCGTCAGGGGGGGAGCCCTATGGAAGAAACGCCAGCA	5596
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QY	4517	TGGCAACAGCTTGGCGAACTATTAACTGCGGAACCTACTTCTAGCTTCCCGCAAC	4576	5597	ACGCGGCTTTTACGCTTCTCGCCCTTTTGTGCGCTTTTGTCTCATCTCTTTCTCTG	5656
Db	1703	TGCCAAACAGCTTGGCGAACTATTAACTGCGGAACCTACTTCTAGCTTCCCGCAAC	1762	2783	ACGCGGCTTTTACGCTTCTCGCCCTTTTGTGCGCTTTTGTCTCATCTCTTTCTCTG	2842
QY	4577	AATTAATAGACTGATGAGCGGATGAAAGTTGAGGACCACTTCTCGCTCGGCCCTTC	4636	5657	CGTTATCCCTGATTTCTGTGATTAACCGTATACCGCTTTTGTGAGTGAAGTACCGCTC	5716
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QY	4637	CGGCTGGCTGTTTATGCTGATAAATCTGGAGCGGTGAGCGTGGGTCTCGCGGTATCA	4696	5717	GCAGCAGCCGAAACGACGAGCGAGTCACTGAGCGAGGAAAGCGGAGAGCGGCCCAA	5776
Db	1823	CGGCTGGCTGTTTATGCTGATAAATCTGGAGCGGTGAGCGTGGGTCTCGCGGTATCA	1882	2903	GCAGCAGCCGAAACGACGAGCGAGTCACTGAGCGAGGAAAGCGGAGAGCGGCCCAA	2962
QY	4697	TTGAGCACTGGGCGCAGATGTAAGCCCTCCGATGCTAGTATCTTACACGAGCGGGA	4756	5777	TAGCAAAACCGCTCTCCCGCGGTTGGCGGATTCAATTAATGCGAG	5822
Db	1883	TTGAGCACTGGGCGCAGATGTAAGCCCTCCGATGCTAGTATCTTACACGAGCGGGA	1942	2963	TAGCAAAACCGCTCTCCCGCGGTTGGCGGATTCAATTAATGCGAG	3008
QY	4757	GTCAGGCACTATGATGAACGAATAGACAGATCGCTGAGATAGGTGCTCACTGATTA	4816	RESULT 2		
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QY	4817	AGCATTTGTAATCTGTACAGCAAGTTTACTCATATATATCTTATGATGATTAATTAACCTC	4876	LOCUS	Expression vector pCOR112N (modified from pCOR112 in [2]).	
Db	2003	AGCATTTGTAATCTGTACAGCAAGTTTACTCATATATATCTTATGATGATTAATTAACCTC	2062	DEFINITION	Z29587	
QY	4877	ATTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTTTGTGATATCTCATGACCAAAATCC	4936	ACCESSION	Z29587.1	GI:452344
Db	2063	ATTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTTTGTGATATCTCATGACCAAAATCC	2122	VERSION	229587.1	GI:452344
QY	4937	CTTAACGTGAGTTTTCGTTCCACTGAGCGTCAAGCCCGGTAGAAAAGATCAAGGATCTT	4996	KEYWORDS	ampicillin resistance; beta-lactamase; coel origin; expression vector; mos terminator; phage fl region; rice actin1 promoter.	
Db	2123	CTTAACGTGAGTTTTCGTTCCACTGAGCGTCAAGCCCGGTAGAAAAGATCAAGGATCTT	2182	SOURCE	synthetic construct	
QY	4997	CTTGAGATCCCTTTTTCGCGCGTAATCTGCTGTGCAAAACCAAAACCAACCGCTAC	5056	ORGANISM	artificial sequences.	
Db	2183	CTTGAGATCCCTTTTTCGCGCGTAATCTGCTGTGCAAAACCAAAACCAACCGCTAC	2242	REFERENCE	1 (bases 27 to 282)	
QY	5057	CAGCGGTGTTTGTGGGATCAAGACTACCACTTTTTCGAGGTAACCTGGCT	5116	AUTHORS	Depicker, A., Stachel, S., Dhaese, P., Zambryski, P. and Goodman, H.M.	
Db	2243	CAGCGGTGTTTGTGGGATCAAGACTACCACTTTTTCGAGGTAACCTGGCT	2302	TITLE	Nopaline synthase: transcript mapping and DNA sequence	
QY	5117	TCAGCAGCGCGAGATACCAATCTCTCTAGTGTAGCGGTAGTTAGGCCACCACT	5176	MEDLINE	J. Mol. Appl. Genet. 1 (6), 561-573 (1982)	
Db	2303	TCAGCAGCGCGAGATACCAATCTCTCTAGTGTAGCGGTAGTTAGGCCACCACT	2362	PUBMED	83110651	
QY	5177	TCAAGAACTCTGTAGCAGCGCTTACATACCTCGCTCTGCTTAATCTCTGTTTACAGTGGCTG	5236	REFERENCE	7153689	
Db	2363	TCAAGAACTCTGTAGCAGCGCTTACATACCTCGCTCTGCTTAATCTCTGTTTACAGTGGCTG	2422	AUTHORS	McElroy, D., Blowers, A.D., Jensen, B. and Wu, R.	
QY	5237	CTGCCAGTGGCGAATAGTGTCTTACCGGGTTGAGCTCAAGACGATAGTTACCGGATA	5296	TITLE	Construction of expression vectors based on the rice actin 1 (Act1) 5' region for use in monocot transformation	
				JOURNAL	Mol. Gen. Genet. 231 (1), 150-160 (1991)	
				MEDLINE	92092956	
				PUBMED	1753941	
				REMARK	(sites)	
				REFERENCE	3 (bases 1 to 4412)	
				AUTHORS	Liu, L., Dasgupta, I., Davies, J.W. and Hull, R.	
				TITLE	Modified vectors for monocot transformation toward virus resistance	
				JOURNAL	Unpublished	
				REFERENCE	4 (bases 1 to 4412)	
				AUTHORS	Liu, L.	
				TITLE	Direct Submission	
				JOURNAL	Submitted (26-JAN-1994) Liu L., John Innes Institute, Virus Research, Colney Lane, Norwich, United Kingdom, NR4 7UH	

FEATURES		Location/Qualifiers
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promoter	3181..4412	/note="rice actin 1 5' region (act1 promoter)"
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ORIGIN		
Query Match		47.4%; Score 2760.8; DB 12; Length 4412;
Best Local Similarity		96.5%; Pred. No. 0;
Matches 2892; Conservative		0; Mismatches 32; Indels 72; Gaps 4;
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QY	2891	GGCTTGGCAGATGATTATCATATAATTTCTGTGCAATTAAGTTAAGCATGTAATAATAC 2950
DB	81	GGCTTGGCAGATGATTATCATATAATTTCTGTGCAATTAAGTTAAGCATGTAATAATAC 140
QY	2951	ATGTAATGATGACGTTATTTATGATGGGTTTTATGATGATGATGATGATGATGATGATG 3010
DB	141	ATGTAATGATGACGTTATTTATGATGGGTTTTATGATGATGATGATGATGATGATGATG 200
QY	3011	ATTTAATAGCGATAGAAACAAATATAGCGCGCAAACTAGGATAAATATGCGCGCG 3070
DB	201	ATTTAATAGCGATAGAAACAAATATAGCGCGCAAACTAGGATAAATATGCGCGCG 260
QY	3071	GTGTCATCTATCTAGATGACCTCGAGCATGGGATCCGCGCGCATGCGGACGTC 3130
DB	261	GTGTCATCTATCTAGATGACCTCGAGCATGGGATCCGCGCGCATGCGGACGTC 310
QY	3131	GGGCGCAATTCGCCCTATAGTGAGTGTATTAC---AATTCACTGGCGGTGTTTTACAA 3187
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QY	3188	CGTCTGACTGGGAAACCTGGCGTTACCAACTAATPCGCTTCGACCAATCCCT 3247
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QY	3248	TTTCGACGCTGGGTAATAGGAGAGCGCGCATCGGATCGCCCTTCCCAAGTGGCG 3307
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QY	3427	TTCCCTTCTCTTCTCGCCACCGTTTCGCGCGCTTTCGCGCTCAAGCTCTAAATCGGGGGTC 3486
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DEFINITION Sequence 3 from patent US 5801027.
ACCESSION AR037157
VERSION AR037157.1 GI:5955013
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 5534)
AUTHORS Bennett M., May, S. and Ramsay, N.
TITLE Method of using transactivation proteins to control gene expression
JOURNAL Patent: US 5801027-A 3 01-SEP-1998;
FEATURES
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VERSION     ARL12043.1  GI:12828891
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SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 5534)
AUTHORS     Bennett, M., May, S. and Ramsay, N.
TITLE       Method of using transactivation proteins to control expression in
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JOURNAL     Patent: US 6127606-A 3 03-OCT-2000;
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Best Local Similarity 96.3%; Pred. No. 0;
Matches 2890; Conservative 0; Mismatches 38; Indels 74; Gaps 4;

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RESULT 5
AF173954/c
LOCUS AF173954 4350 bp DNA circular SYN 01-OCT-1999
DEFINITION Cloning vector pGEM-URA3, complete sequence.
ACCESSION AF173954
VERSION AF173954.1 GI:6002958
KEYWORDS
SOURCE Cloning vector pGEM-URA3
ORGANISM Cloning vector pGEM-URA3
REFERENCE 1 (bases 1 to 4350)
AUTHORS Wilson,R.B., Davis,D. and Mitchell,A.P.
TITLE Rapid hypothesis testing with Candida albicans through gene disruption with short homology regions
JOURNAL J. Bacteriol. 181 (6), 1868-1874 (1999)
MEDLINE 99173911
PUBMED 10074081
REFERENCE 2 (bases 1 to 4350)
AUTHORS Wilson,R.B., Davis,D. and Mitchell,A.P.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-1999) Microbiology, Columbia University, 701 W. 168th St., New York, NY 10032, USA
FEATURES
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AF173955/c
LOCUS AF173955 5558 bp DNA circular SYN 01-OCT-1999
DEFINITION Cloning vector pGEM-HIS1, complete sequence.
ACCESSION AF173955
VERSION AF173955.1 GI:6002960
KEYWORDS

SOURCE

Cloning vector pGEM-HIS1
Cloning vector pGEM-HIS1
artificial sequences; vectors.
1 (bases 1 to 5558)
REFERENCE
AUTHORS Wilson, R.B., Davis, D. and Mitchell, A.P.
TITLE Rapid hypothesis testing with Candida albicans through gene
disruption with short homology regions
J. Bacteriol. 181 (6), 1868-1874 (1999)
MEDLINE 99173911
PUBMED 10074081

REFERENCE 2 (bases 1 to 5558)
AUTHORS Wilson, R.B., Davis, D. and Mitchell, A.P.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-1999) Microbiology, Columbia University, 701 W.
168th St., New York, NY 10032, USA
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ORIGIN
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 2707; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 2960 CGGAGCATCGCAGCTCGGCCCAATTCGCGCTATAGTAGTGTATTAACAATTCACCTGG 2901
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Db |||||

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1460	Db	ACCACTTCTGCGCTCGGCCCTTCGCGGTGCGCTGTTTATGCTGATAAATCTGGAGCCG	1401
4674	Qy	TGAGCGTGGGTCTCGCGGTATCATGACGACTCGGCGCATGCTGAAGCCCTCCCGTAT	4733
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RESULT 7
E63777/C

1280	TGAGATAGGTGGCTCACTCAATTAAGCAATTTGGTAACTGTGCAGACCAAGTTTACTCATATAT	1221
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5814 TTAATGCAG 5822

260 TTAATGCAG 252

LOCUS E63777 4229 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for assaying the stability of genetic information in animal cells.
ACCESSION E63777
VERSION E63777.1 GI:22553615
KEYWORDS JP 2001087000-A/5.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 4229).
AUTHORS Nakanishi, M. and Ikawa, Y.
TITLE Method for assaying the stability of genetic information in animal
JOURNAL Patent: JP 2001087000-A 5 03-APR-2001;
COMMENT KK SENTAN KAGAKU GIJYU-SU INCUBATION CENTER
OS Artificial Sequence
PN JP 2001087000-A/5
PD 03-APR-2001
PF 17-SEP-1999 JP 1999264320
PI MASATO NAKANISHI, YUMI IKAWA
PC C12Q1/68, C12N5/10, C12N15/09, C12Q1/04//A61K48/00, C12N5/00, PC
C12N15/00
CC Restriction enzyme BamHI-cut site
CC Restriction enzyme SmaI-cut site
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Matches 2686; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION		Sequence 6 from Patent WO02086100.	
ACCESSION	AX590988		
VERSION	AX590988.1	GI:27949532	
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1		
AUTHORS	Bosman,A., Depla,E., Deschamps,G., Sablon,E., Samson,I., van Broekhoven,A. and Haelewyn,J.		
TITLE	Expression of core-glycosylated hcv envelope proteins in yeast		
JOURNAL	Patent: WO 02086100-A 6 31-OCT-2002; INNOGENETICS N.V. (BE)		
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	Matches 2693; Conservative 0; Mismatches 16; Indels 0; Gaps 0;		
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QY	3174	CCGTGCGTTTACAACTGTCGACCTGGGAAAACCCCTGCGTTTACCCAACTTAATCGCCTTG	3233
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QY	3234	CAGCACATCCCCCTTTCCGACGCTGGCGTAATAGCGAAGGCGCCGACCGATCGCCCTT	3293
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QY	3354	GGCGGGTGTGTGGTTTACGCGCAGCGCTGACCGCTTACCTTGCCAGCGCCCTAGCGCCCGC	3413
Db	2745	GGCGGGTGTGTGGTTTACGCGCAGCGCTGACCGCTTACCTTGCCAGCGCCCTAGCGCCCGC	2686
QY	3414	TCCTTTGCTTTTCTTCCCTTCTTCTGCGCACGCTTCCCGCGCTTCCCGCTCAAGCTCT	3473
Db	2685	TCCTTTGCTTTTCTTCCCTTCTTCTGCGCACGCTTCCCGCGCTTCCCGCTCAAGCTCT	2626
QY	3474	AAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGAGCTTTAGCGACCTTCGACCGCAAAA	3533
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QY	3534	ACTTGATTTGGGTGATGGTTTACGCTAGTGGGCCATCGCCCTGTAGAGCGGTTTTTCGCC	3593
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QY	3594	TTTGACGTTGGAGTCCAGGTTCTTTAATAGTGGACTCTGTGTTCCTTCCAACTTGAACACACT	3653
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QY	3654	CAACCTTATCTCGGCTATCTTTTGAATTAAGGATTTTTCGGATTTTCGGCTATTG	3713
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QY	3714	GTTAAAAAATGAGCTGATTTTAAACAAATTTTAAACGCGAATTTTAAACAAATATTACGTT	3773
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QY	4937	CTTAACGCTGAGTTTTCGTTCCACTGACGCTCGACCCCTGAGAAAGATCAAGAGATCTT	4996
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QY	4997	CTTGAGATCTTTTTCCTGCGGTAATCTGCTGCTTGCAAAACAAAAACACCGCTAC	5056
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QY	5057	CAGCGGTGGTTTGTTCGCGGATCAAGAGCTACCAACTCTTTTTCGGAAGGTAACTGGCT	5116
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QY	5237	CTGCGAGTGGCGATAGTCTGTCTTACCGGGTTGGACTCAAGACGATAGTACCAGGATA	5296
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Db	997	AGGCGCAGCGCTCGGCTGAAACGGGGGTTCTGTCACACAGCCCGACTTCGAGCGCAACGA	938
QY	5357	CCTACACCGAACTGAGATACTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAG	5416
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QY	5777	TACGAAACCGGCTCTCCCGGGGTTGGCGGATTCATTAATGAG	5822
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RESULT 8
AX590988/c
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AX590988

3448 bp DNA linear PAT 27-JAN-2003

RESULT 8

AX590988/c

LOCUS

3448 bp DNA linear PAT 27-JUN-2003

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RESULT 9
AX591141/c

LOCUS

AX591141
Sequence 6 from Patent WO02085932.
linear PAT 27-JAN-2003

DEFINITION

AX591141

ACCESSION

VERSION

AX591141.1

GI:27949651

KEYWORDS

synthetic construct

SOURCE

ORGANISM

artificial sequences.	
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REFERENCE	Sablon,E., van Broekhoven,A., Bosman,A., Depla,E. and Deschamps,G.
AUTHORS	Constructs and methods for expression of recombinant hcv envelope
TITLE	proteins
JOURNAL	Patent: WO 02085932-A 6 31-OCT-2002;
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Best Local Similarity	99.4%; Pred. No. 0;
Matches 2693; Conservative	0; Mismatches 16; Indels 0; Gaps 0;
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Db	2865 CAGCACATCCCCCTTCGCCAGCTGGCGTAATAGCAAGAGGCGCCGACGGATCGCCCTT 2806
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Db	2805 CCCAAAGTTGCGCAGCCTGAATGGCGAAATGGACGCGGCCCTGTAGCGGGCGCATTAAGCGC 2746
QY	3354 GCGCGGTGGTGGTTACGCGAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGC 3413
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QY	3474 AAATCGGGGGCTCCCTTTAGGGTTCGATTTAGAGCTTTACGGCACTCGACCGCAAAA 3533
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	SOURCE	Expression vector pCMH285		
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		artificial sequences; vectors.		

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Db 3472 TTAATGCAG 3480

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RESULT 13
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DEFINITION
  CVGEM7LICF 3033 bp DNA circular SYN 16-MAY-1995
  Ligation-independent cloning vector pGEM-7Zf(+)/LIC-F, complete
  sequence.
ACCESSION
  U25272
VERSION
  U25272.1 GI:806889
KEYWORDS
  beta-lactamase; ligation-independent cloning region; Nari
  restriction site.
SOURCE
  Cloning vector pGEM-7Zf(+)/LIC-F
  Cloning vector pGEM-7Zf(+)/LIC-F
  artificial sequences; vectors.
ORGANISM
  1 (bases 1 to 3033)
  Haun,R.S., Serventi,I.M. and Moss,J.
REFERENCE
  1 Rapid, reliable ligation-independent cloning of PCR products using
  modified plasmid vectors
  Biotecniques 13 (4), 515-518 (1992)
MEDLINE
  93119606
PUBMED
  1362067
REFERENCE
  2 (bases 1 to 3033)
  Haun,R.S.
  Direct Submission
  Submitted (19-APR-1995) Randy S. Haun, NIH, NHLBI, Laboratory of
  Cellular Metabolism, Bldg. 10, Room 5N307, Bethesda, MD 20892-1434,
  USA
COMMENT
  Ligation-independent cloning vector. Preparation of the vector for
  cloning includes linearization with Nari, gel purification of the
  linearized vector, and treatment with T4 DNA polymerase in the
  presence of dATP. The target sequence can be amplified using
  sequence specific primers modified at the 5' end to contain an
  additional 13 nucleotides complementary to the vector. The forward
  primer should contain 5'-CTGGTCCGGCA-3', followed by 12-15
  nucleotide target-specific sequence. The reverse primer should
  contain 5'-CTCGTCCGGCA-3', followed by 12-15 nucleotide
  target-specific sequence. The amplified sequence should be gel
  purified and treated with T4 DNA polymerase in the presence of
  dATP. Annealing of the vector and the amplification product forms a
  duplex that can be used directly for transformation. Sequences
  amplified using these primers are also compatible with the
  pBluescript II KS(+)/LIC vector (ATCC 87047) and pGEM-7Zf(+)/LIC-R
  vector (ATCC 87049). Differs from pGEM-7Zf(+)/LIC-R (ATCC 87049)
  only in the orientation of complementary ends generated at the
  cloning site. This vector has been deposited in the ATCC repository
  (ATCC 87048).
FEATURES
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 5786 CGCCTCTCCCCCGCGGTTTGGCGGATTCAATTAATGCA 5822
Db 393 CGCCTCTCCCCCGCGGTTTGGCGGATTCAATTAATGCA 357

RESULT 14
CVGM7LICR/c

LOCUS CVGM7LICR 3033 bp DNA circular SYN 16-MAY-1995
DEFINITION Ligation-independent cloning vector pGEM-7zf(+)/LIC-R, complete sequence.

ACCESSION U25268
VERSION U25268.1
KEYWORDS beta-lactamase; ligation-independent cloning region; NarI restriction site.

SOURCE Cloning vector pGEM-7zf<+>/LIC-R
ORGANISM artificial sequences; vectors.
1 (bases 1 to 3033)

REFERENCE Haun, R.S., Serventi, I.M. and Moss, J.
AUTHORS Rapid, reliable ligation-independent cloning of PCR products using modified plasmid vectors

TITLE BioTechniques 13 (4), 515-518 (1992)
JOURNAL MEDLINE 93119606
PUBMED 1362067

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2004, 09:30:17 ; Search time 1367 Seconds
(without alignments)
18092.911 Million cell updates/sec

Title: US-09-924-197-1

Perfect score: 5822

Sequence: 1 ctggcagacaggttcccg.....tgccgattcattaatgacg 5822

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001as.*
- 5: Geneseq2001bs.*
- 6: Geneseq2002s.*
- 7: Geneseq2003as.*
- 8: Geneseq2003bs.*
- 9: Geneseq2003cs.*
- 10: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5822	100.0	5822	6 AAS20853	Expresio
2	2757.2	47.4	5534	2 AAT43137	Aat43137 pUMIGIT s
3	2686	46.1	4229	4 AAH25896	Genetic i
4	2683.4	46.1	3448	7 ABQ84197	Abq84197 Vector pG
5	2683.4	46.1	3448	7 AAD50589	pGEMTEISH
6	2680.4	46.0	3448	7 ABT14439	HCV envel
7	2675.4	46.0	3018	2 AAX22905	Plasmid p
8	2675.4	46.0	5919	4 AAD09980	pHSP-GUS
9	2670.2	45.9	3357	7 ACC44700	Plasmid p
10	2670.2	45.9	3357	7 ABT16597	Artificia
11	2668.6	45.8	4514	8 ADA94775	Plasmid p
12	2658.4	45.7	9359	6 ABK11039	pVDH636 v
13	2658.4	45.7	9359	6 ABK10687	Transfom
14	2641.4	45.4	3404	8 ADA41728	Plasmid p
15	2634.4	45.2	3968	4 AAD09981	pHSP70-1M
16	2634.4	45.2	4626	4 AAD09988	pHSP-ohox
17	2630.4	45.2	3485	6 AAI72813	Expresio
18	2553	43.9	4965	2 AAV18742	Complete
19	2553	43.9	5109	2 AAV13846	Complete
20	2553	43.9	6196	2 AAV13168	Complete
21	2553	43.9	6243	2 AAV13841	Complete
22	2553	43.9	6503	2 AAV13169	Complete
23	2553	43.9	6959	2 AAV13165	Complete

C 24	2553	43.9	7379	2	AAV13176	Complete
C 25	2553	43.9	8792	2	AAV18745	Complete
C 26	2552	43.8	10078	6	ABQ73047	Tomato an
C 27	2551.8	43.8	37808	2	AAX02780	Vector pM
C 28	2551.4	43.8	8618	2	AAV18741	Complete
C 29	2550	43.8	4883	6	AAD28233	CMV expre
C 30	2550	43.8	7287	2	AAV02042	Plasmid p
C 31	2549.4	43.8	2962	9	ADD14879	Phage dis
C 32	2549.4	43.8	3057	9	ADD14892	Phage dis
C 33	2549.4	43.8	3093	4	ADD14876	Phage dis
C 34	2549	43.8	2958	4	AAS13970	Plasmid p
C 35	2549	43.8	2958	4	AAS13969	Plasmid p
C 36	2549	43.8	2958	4	AAS13971	Plasmid p
C 37	2549	43.8	3351	6	ABT08167	Recombina
C 38	2549	43.8	4754	6	ABT08175	Recombina
C 39	2549	43.8	4773	6	ABT08176	Recombina
C 40	2549	43.8	4831	6	ABT08194	Recombina
C 41	2549	43.8	6345	2	AAX88054	Plasmid p
C 42	2549	43.8	21329	7	AAD48562	Chimeric
C 43	2545.8	43.7	6046	2	AAV13845	Complete
C 44	2545.8	43.7	6245	2	AAV13844	Complete
C 45	2545.8	43.7	6448	2	AAV13843	Complete

ALIGNMENTS

RESULT 1

AAS20853
ID AAS20853 standard; DNA; 5822 BP.

XX AAS20853;

DT 05-JUN-2002 (first entry)

XX Expression cassette, pFP-IRN1 useful for gene silencing.

KW Inhibition of gene expression; expression cassette; inverted repeat; IR;
KW NOS; nopaline synthase; figwort mosaic virus promoter; FMV; hsp70; PG;
KW plant heat shock 70; tomato; polygalacturonase; disease resistance;
KW flavour; nutritional characteristic; plant; gene silencing; pFP-IRN1;
KW regulating gene expression; mutant; ds.

XX Lycopersicon esculentum.

OS Agrobacterium tumefaciens.

OS Figwort mosaic virus.

OS Synthetic.

OS Chimeric.

PN WO200214472-A2.

XX 21-FEB-2002.

XX 14-AUG-2001; 2001WO-US025538.

XX 15-AUG-2000; 2000US-0225508P.

XX 07-AUG-2001; 2001US-00924197.

XX (DNAP) DNA PLANT TECHNOLOGY CORP.

XX Gutterson N, Oeller P;

XX WPI; 2002-257599/30.

XX Reducing the expression of a target gene in a cell, comprises expressing
PT in the cell an expression cassette comprising a promoter operably linked
PT to a sense or antisense targeting sequence and an inverted repeat of a
PT nopaline synthase gene.

XX Claim 51; Page 37-39; 39pp; English.

XX The present invention relates to an improved method for inhibiting the
CC expression of a target gene in a cell, by expressing in the cell an

CC expression cassette comprising a promoter operably linked to a sense or
CC antisense targeting sequence having substantial identity to a subsequence
CC of the target gene, and an inverted repeat (IR) of a subsequence of a NOS
CC (nopaline synthase) gene, where the IR is unrelated to the targeting
CC sequence. The expression cassette, pFP-IRN1 is constructed using a
CC figwort mosaic virus (FMV) promoter in which the 5'-untranslated leader
CC (5'-UTL) is derived from a plant heat shock 70 (hsp70) gene, the tomato
CC polygalacturonase (PG) gene and an IR of the terminator of the
CC Agrobacterium tumefaciens NOS gene. The method is useful for regulating
CC expression of endogenous genes and transgenes, e.g. to regulate
CC expression of endogenous plant phenotypes, such as disease resistance,
CC flavour, protein or nutritional characteristics. The improved gene
CC silencing construct is used in functional genomics to determine the
CC effect of regulating gene expression of a selected endogenous gene or
CC transgene. The method is simple and rapid, and is suitable for high-
CC throughput studies. Multiple transgenic constructs all containing the
CC same repeat element can be silenced at the same time, since the initial
CC silencing trigger mediated through the inverted repeat region will apply
CC to all of the transcripts. The present sequence represents the expression
CC cassette, pFP-IRN1
XX

Sequence 5822 BP; 1689 A; 1275 C; 1292 G; 1566 T; 0 U; 0 Other;

Query Match 100.0%; Score 5822; DB 6; Length 5822;

Best local Similarity 100.0%; Pred. No. 0;

Matches 5822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CTGGCAGCAGGTTTCCCGACCTGGAAAGCGGCGAGTGGCGCAACCAATTATGTGAG	60
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DB	61	TTAGCTCAGCTCATTAGGACCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTG	120
QY	121	TGGAATTTGAGCGGATACAAATTTACAGGAAACAGCTATGACCATGATTACGCCAA	180
DB	121	TGGAATTTGAGCGGATACAAATTTACAGGAAACAGCTATGACCATGATTACGCCAA	180
QY	181	GCTATTTAGTGACACTATAGATCTCAAGCTATGATCCAAAGCTTGGAGCTCTCC	240
DB	181	GCTATTTAGTGACACTATAGATCTCAAGCTATGATCCAAAGCTTGGAGCTCTCC	240
QY	241	CATATGCTGCAGCTGCAGCGCGCGCACTAGTATGCTTGAATCTCGAGTGGAGCTAAT	300
DB	241	CATATGCTGCAGCTGCAGCGCGCGCACTAGTATGCTTGAATCTCGAGTGGAGCTAAT	300
QY	301	TCTCAGTCCAAAGCCTCAACAAGTCAAGGTACAGAGTCTCCAAACCATTAGCCAAAGC	360
DB	301	TCTCAGTCCAAAGCCTCAACAAGTCAAGGTACAGAGTCTCCAAACCATTAGCCAAAGC	360
QY	361	TACAGGAGATCAATGAAGATCTTCAATCAAAGTAAACTACTGTTCAGACACATGCATCA	420
DB	361	TACAGGAGATCAATGAAGATCTTCAATCAAAGTAAACTACTGTTCAGACACATGCATCA	420
QY	421	TGCTCAGTAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCACTTTG	480
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QY	481	AAAGTAATCTGTCAACATCGAGCAGCTGGCTGTGGGGACACAGCAAAAAGGAATGGT	540
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DB	541	GCAGAAATGTTAGCGCACCTTACCAAAAGCATCTTTGCCCTTTATTTGCAAAAGATAAGCAG	600
QY	601	ATTCTCTAGTACAAAGTGGGAAACAAATTAACGTGGAAAGAGCTGTCGACAGCCAC	660
DB	601	ATTCTCTAGTACAAAGTGGGAAACAAATTAACGTGGAAAGAGCTGTCGACAGCCAC	660
QY	661	TCAGTAATGCGTATGACGAGCGAGTGCAGCCACCAAGAAATTTAGCTTGAGCTCAGAT	720
DB	661	TCAGTAATGCGTATGACGAGCGAGTGCAGCCACCAAGAAATTTAGCTTGAGCTCAGAT	720

DB	661	TCAGTAATGCGTATGACGAGCGAGTGCAGCCACCAAGAAATTTAGCTTGAGCTCAGAT	720
QY	721	TTAGCAGCATTCAGAGATTTGGGTTCAATCAACAAGGTACGAGCCATATCACTTTATTCAAA	780
DB	721	TTAGCAGCATTCAGAGATTTGGGTTCAATCAACAAGGTACGAGCCATATCACTTTATTCAAA	780
QY	781	TTGGTATCGCAAAAACAAGAGAACTCCATCTCTCAAGGTTTGTAAAGAAATCTT	840
DB	781	TTGGTATCGCAAAAACAAGAGAACTCCATCTCTCAAGGTTTGTAAAGAAATCTT	840
QY	841	CAGTCCAAAGCCTCAACNAGTCAAGGTACAGGTCTCCAAACCATTTAGCCAAAGCTAC	900
DB	841	CAGTCCAAAGCCTCAACNAGTCAAGGTACAGGTCTCCAAACCATTTAGCCAAAGCTAC	900
QY	901	AGGAGATCAATGAAGATCTTCAATCAAAAGTAAACTCTGTTCCAGCACATGATCATGG	960
DB	901	AGGAGATCAATGAAGATCTTCAATCAAAAGTAAACTCTGTTCCAGCACATGATCATGG	960
QY	961	TCAGTAAGTTTCAGAAAAAGACATCCACCGAAGCTTAAAGTTAGTGGGCACTTTGAAA	1020
DB	961	TCAGTAAGTTTCAGAAAAAGACATCCACCGAAGCTTAAAGTTAGTGGGCACTTTGAAA	1020
QY	1021	GTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGACACAGACAAAAAGAAATGGTGCA	1080
DB	1021	GTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGACACAGACAAAAAGAAATGGTGCA	1080
QY	1081	GAATTTGTAGCGCACCTTACCAAAAGCATCTTTGCCCTTTATTTGCAAAAGATAAGCAGAT	1140
DB	1081	GAATTTGTAGCGCACCTTACCAAAAGCATCTTTGCCCTTTATTTGCAAAAGATAAGCAGAT	1140
QY	1141	CCTCTAGTACAAAGTGGGAAACAAATTAACGTGGAAAGAGCTGTCTCTATATAAGAGGCA	1200
DB	1141	CCTCTAGTACAAAGTGGGAAACAAATTAACGTGGAAAGAGCTGTCTCTATATAAGAGGCA	1200
QY	1201	CTAATCGTATGACGAGCAGTACGACCAACAAAGAAATTCCTCTCTATATAAGAGGCA	1260
DB	1201	CTAATCGTATGACGAGCAGTACGACCAACAAAGAAATTCCTCTCTATATAAGAGGCA	1260
QY	1261	TTCAATTCCTTTCAGAGGACACAGAAAAATTTGCTACATTTGTTTCAAAACTTCAAAATAT	1320
DB	1261	TTCAATTCCTTTCAGAGGACACAGAAAAATTTGCTACATTTGTTTCAAAACTTCAAAATAT	1320
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DB	1321	TATTCATTTATTTGTGACGCTTTCAAACTCTTTGTTTCTGTTTGTGTTGAGTATATTT	1380
QY	1381	AAAAACATGCTTCTTAAAAACAAGATTTATCTTCTCAAGCAAAATCACTTTTCAGGTCCA	1440
DB	1381	AAAAACATGCTTCTTAAAAACAAGATTTATCTTCTCAAGCAAAATCACTTTTCAGGTCCA	1440
QY	1441	TGCAGATCTTCTATTTTCAGTAAAGATTTTGGATCTTTAGAGCATCTAGTAAATTTCA	1500
DB	1441	TGCAGATCTTCTATTTTCAGTAAAGATTTTGGATCTTTAGAGCATCTAGTAAATTTCA	1500
QY	1501	GACTACAAAGATAGAGGCTTTGGATGCTTTTGTATGATGTTTCAAAATTTAGTGTGGA	1560
DB	1501	GACTACAAAGATAGAGGCTTTGGATGCTTTTGTATGATGTTTCAAAATTTAGTGTGGA	1560
QY	1561	GGAGGAGAACTATCAATGCAAGTATGGTGGCCAAAGTCTCTGCAAAATAAAT	1620
DB	1561	GGAGGAGAACTATCAATGCAAGTATGGTGGCCAAAGTCTCTGCAAAATAAAT	1620
QY	1621	AAATCACTGCGAGGATGCACCAACCGGCTTAACTCTGGAATTTGCAAAAATTTG	1680
DB	1621	AAATCACTGCGAGGATGCACCAACCGGCTTAACTCTGGAATTTGCAAAAATTTG	1680
QY	1681	AAAGTGAATTAATCTTAAGAGTAAATTCACAAATTCATATCAATTTGAGTCATGC	1740
DB	1681	AAAGTGAATTAATCTTAAGAGTAAATTCACAAATTCATATCAATTTGAGTCATGC	1740
QY	1741	ACTAATCTTGTAGCTTCAAAATTTGATGATCAATGCTTTCAGCAAAAGAGCCCAAAATCTGAT	1800
DB	1741	ACTAATCTTGTAGCTTCAAAATTTGATGATCAATGCTTTCAGCAAAAGAGCCCAAAATCTGAT	1800

Db 3961 AAGAGTATGAGTATCAACATTTCCGTGTCGCCCTTATTCCCTTTTGTGGCATTTTGC 4020
QY 4021 CTTCTCTGTTTTCTCACCCAGAAAACGCTGGTGAAGTAAAGATGCTGAAGATCAGTTG 4080
Db 4021 CTTCTCTGTTTTCTCACCCAGAAAACGCTGGTGAAGTAAAGATGCTGAAGATCAGTTG 4080
QY 4081 GGTGCAGAGTGGTTTACATCGAACTGGATCTCAACAGCGGTAAAGTCTTTGAGAGTTTT 4140
Db 4081 GGTGCAGAGTGGTTTACATCGAACTGGATCTCAACAGCGGTAAAGTCTTTGAGAGTTTT 4140
QY 4141 CGCCCGAAGAACGTTTTCAATGATGAGACACTTTTAAAGTCTCTATGTCGCGGTA 4200
Db 4141 CGCCCGAAGAACGTTTTCAATGATGAGACACTTTTAAAGTCTCTATGTCGCGGTA 4200
QY 4201 TTATCCCGTATTGACGCGCGGCAAGAGCAACTCGGTCCGCGCATACACTATTCTCAGAAT 4260
Db 4201 TTATCCCGTATTGACGCGCGGCAAGAGCAACTCGGTCCGCGCATACACTATTCTCAGAAT 4260
QY 4261 GACTTGGTTGAGTACTACACAGTCAAGAAAAGCATCTTACCGATGGCATGACAGTAAGA 4320
Db 4261 GACTTGGTTGAGTACTACACAGTCAAGAAAAGCATCTTACCGATGGCATGACAGTAAGA 4320
QY 4321 GAATATGAGTCTGTCGATTAACCATGAGTGATAACACTGCGGCGCAACTTACTCTGACA 4380
Db 4321 GAATATGAGTCTGTCGATTAACCATGAGTGATAACACTGCGGCGCAACTTACTCTGACA 4380
QY 4381 ACCATCGAGGACCGAAGAGAGTAAACCGCTTTTTTGCACAACATGGGGATCATGTAAC 4440
Db 4381 ACCATCGAGGACCGAAGAGAGTAAACCGCTTTTTTGCACAACATGGGGATCATGTAAC 4440
QY 4441 CGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAACAGCAGCGTGACACC 4500
Db 4441 CGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAACAGCAGCGTGACACC 4500
QY 4501 ACCATCGCTAGCAATGGCAACACGTTGCGCAACTATTAACTGCGCACTACTTACT 4560
Db 4501 ACCATCGCTAGCAATGGCAACACGTTGCGCAACTATTAACTGCGCACTACTTACT 4560
QY 4561 CTAGCTTCCCGCAACAAATTAATAGACTGGATGGAGCGGATAAAGTTGCGAGCACACT 4620
Db 4561 CTAGCTTCCCGCAACAAATTAATAGACTGGATGGAGCGGATAAAGTTGCGAGCACACT 4620
QY 4621 CTGCGTCTGCGCCCTTCCGCTGGCTGTTTATCTGATAAATCTGAGCCGCTGAGCGT 4680
Db 4621 CTGCGTCTGCGCCCTTCCGCTGGCTGTTTATCTGATAAATCTGAGCCGCTGAGCGT 4680
QY 4681 GGGTCTCGCGTATCATTCAGCACTGGGCGCAGATGGTAAGCCCTCCGATCTAGTT 4740
Db 4681 GGGTCTCGCGTATCATTCAGCACTGGGCGCAGATGGTAAGCCCTCCGATCTAGTT 4740
QY 4741 ATCTACACGACGGGAGTCAAGCAACTATGGATGAACGAATAGACAGATCGCTGAGATA 4800
Db 4741 ATCTACACGACGGGAGTCAAGCAACTATGGATGAACGAATAGACAGATCGCTGAGATA 4800
QY 4801 GGTGCTCTACTGATTAAGCAATGGTAACTGTCTAGACCAAGTTTACTCATATATCTTTAG 4860
Db 4801 GGTGCTCTACTGATTAAGCAATGGTAACTGTCTAGACCAAGTTTACTCATATATCTTTAG 4860
QY 4861 ATTGATTTAAACCTTCATTTTAAATTAAGAGATCTAGTGAAGATCCTTTTGTATAAT 4920
Db 4861 ATTGATTTAAACCTTCATTTTAAATTAAGAGATCTAGTGAAGATCCTTTTGTATAAT 4920
QY 4921 CTCATGACCAAAATPCCCTTAACTGAGTTTTCGTTCCATCTGAGCGTCAGACCCCGTAGAA 4980
Db 4921 CTCATGACCAAAATPCCCTTAACTGAGTTTTCGTTCCATCTGAGCGTCAGACCCCGTAGAA 4980
QY 4981 AAGATCAAGAGATCTCTGAGATCCTTTTTTCTGGCGGTAATCTGCTGCTGCAACA 5040
Db 4981 AAGATCAAGAGATCTCTGAGATCCTTTTTTCTGGCGGTAATCTGCTGCTGCAACA 5040
QY 5041 AAAAAACCCGCTTACAGCGGTGTTGTTTCGCGATCAAGAGCTACCACTCTTTT 5100

Db 5041 AAAAAACCCGCTTACAGCGGTGTTGTTTGTCCGATCAAGAGCTACCACTCTTTT 5100
QY 5101 CCGAAGTAACTGGCTTTCAGCAGAGCGAGATACCAATACTCTCTCTCTAGTGTAGCG 5160
Db 5101 CCGAAGTAACTGGCTTTCAGCAGAGCGAGATACCAATACTCTCTCTAGTGTAGCG 5160
QY 5161 TAGTTAGGCACCACTTCAAGAACTCTGTAGCAACCGCTTACATCTCTCTGCTAATC 5220
Db 5161 TAGTTAGGCACCACTTCAAGAACTCTGTAGCAACCGCTTACATCTCTCTGCTAATC 5220
QY 5221 CTGTTACCACTGCTCTGCTGAGTAACTCTGCTTACCGGTTTGGACTCAAGA 5280
Db 5221 CTGTTACCACTGCTCTGCTGAGTAACTCTGCTTACCGGTTTGGACTCAAGA 5280
QY 5281 CGATAGTTACCGGATTAAGCGCAGCGCTGGGCTGAACCGGGGTTCTGTCACACAGCCC 5340
Db 5281 CGATAGTTACCGGATTAAGCGCAGCGCTGGGCTGAACCGGGGTTCTGTCACACAGCCC 5340
QY 5341 AGTTTGGAGGAAACGACCTTACCGAACTGAGATACCTTACAGGTGAGCTTATGAGAA 5400
Db 5341 AGTTTGGAGGAAACGACCTTACCGAACTGAGATACCTTACAGGTGAGCTTATGAGAA 5400
QY 5401 GCCACGCTTCCGAAAGGAGAAAGCGGACAGGTATCCGCTAAGCGGACGGTTCGGAACA 5460
Db 5401 GCCACGCTTCCGAAAGGAGAAAGCGGACAGGTATCCGCTAAGCGGACGGTTCGGAACA 5460
QY 5461 GGAGAGCGCACGAGGAGCTTCCAGGGGAAACGCTGCTATCTTTATATGCTCTGTCGG 5520
Db 5461 GGAGAGCGCACGAGGAGCTTCCAGGGGAAACGCTGCTATCTTTATATGCTCTGTCGG 5520
QY 5521 TTTTGGCACTCTGACTTGGAGCGTATTTTGTGATGCTCTGTCAGGGGGCGGAGCCTA 5580
Db 5521 TTTTGGCACTCTGACTTGGAGCGTATTTTGTGATGCTCTGTCAGGGGGCGGAGCCTA 5580
QY 5581 TGCAAAAACCGCAGCAACCGCGCTTTTACGCTTCTGCTGCTTGTGCTGCTGCTGCTGCT 5640
Db 5581 TGCAAAAACCGCAGCAACCGCGCTTTTACGCTTCTGCTGCTTGTGCTGCTGCTGCTGCT 5640
QY 5641 CACATGCTCTTCTGCTGCTTATCCCTGATTTCTGTGATTAACCGTATTAACCGCTTTGAG 5700
Db 5641 CACATGCTCTTCTGCTGCTTATCCCTGATTTCTGTGATTAACCGTATTAACCGCTTTGAG 5700
QY 5701 TGAGCTGATACCGCTCGCGCAGCGCAACGACGAGCGCAGCGAGTCAGTGAGGAGGAA 5760
Db 5701 TGAGCTGATACCGCTCGCGCAGCGCAACGACGAGCGCAGCGAGTCAGTGAGGAGGAA 5760
QY 5761 GCGGAAGAGCGCCCAATACGCAACCGCTCTCCCGCGGTTGGCGGATTCATTATGTC 5820
Db 5761 GCGGAAGAGCGCCCAATACGCAACCGCTCTCCCGCGGTTGGCGGATTCATTATGTC 5820
QY 5821 AG 5822
Db 5821 AG 5822

RESULT 2
AAT43137
ID AAT43137 standard; DNA; 5534 BP.
XX
AC AAT43137;
XX
DT 10-FEB-1997 (first entry)
XX
pUMIGIT sequence including upstream activating sequence.
XX
Transgenic plant; gene expression; upstream activating sequence; UAS;
transactivating protein; Gal4; herbicide resistance; polyhydroxybutyrate;
safety; pUMIGIT; ds.
XX
OS
XX
Synthetic.
XX
PN CA2150039-A.
XX

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PD 09-AUG-1996.
XX
XX
XX 24-MAY-1995; 95CA-02150039.
XX
XX 08-FEB-1995; 95GB-00002456.
XX
XX (UYWA-) UNIV WARWICK.
XX
XX Bennett M, May S, Ramsay N;
XX
XX WPI; 1996-486150/49.
XX
XX Control of genes in transgenic plants - using an upstream activating
XX sequence activated by a transactivating protein expressed using a
XX separate promoter.
XX
XX Example; Fig 5F; 48pp; English.
XX
XX Reporter plasmid pUMIGIT (AAT43137), or pUAS Minimal promoter Gus Int
XX Terminator, contains a beta-glucuronidase (GUS) reporter gene under the
XX control of the 46S cauliflower-mosaic virus minimal promoter and 10
XX synthetic 17-bp GAL4 binding sites. The upstream activating sequence
XX (UAS) of pUMIGIT is activatable by yeast transactivating protein GAL4. In
XX a novel method for controlling gene expression, a first transgenic plant
XX carrying a gene encoding a desired phenotype (herbicide resistance of
XX polyhydroxybutyrate prodn.) operatively linked to a UAS recognition site
XX is pollinated by a second transgenic plant carrying Gal4 DNA (see also
XX AAT43136). The transgene is fully expressed in F1 hybrid plants but
XX segregates apart in subsequent generations, improving environmental
XX safety
XX
XX Sequence 5534 BP; 1400 A; 1355 C; 1387 G; 1363 T; 0 U; 29 Other;
XX
XX
XX Query Match 47.4%; Score 2757.2; DB 2; Length 5534;
XX Best Local Similarity 96.3%; Pred. No. 0;
XX Matches 2891; Conservative 0; Mismatches 37; Indels 74; Gaps 4;
XX
XX QY 2840 GATCGTTCAACATTTGSCAATAAAGTTCTTAAGATTGAATCCTGTGCGGTCCTGCG 2899
XX DB 2366 GATCGTTCAACATTTGSCAATAAAGTTCTTAAGATTGAATCCTGTGCGGTCCTGCG 2425
XX
XX QY 2300 ATGATTATCATATATTTCTGTTCAATTAACGTTAAGCATGTAATAATTAACATGTAATGC 2959
XX DB 2426 ATGATTATCATATATTTCTGTTCAATTAACGTTAAGCATGTAATAATTAACATGTAATGC 2485
XX
XX QY 2360 ATGACGTTATTTATGAGATGGTTTTTATGATTAGATCCCGCAATTAATTAACATTAATAC 3019
XX DB 2486 ATGACGTTATTTATGAGATGGTTTTTATGATTAGATCCCGCAATTAATTAACATTAATAC 2545
XX
XX QY 3020 GCGATAGAAAACAAATATAGCGGCAAACTAGGATTAATTAATCGCGCGGTGTCATCT 3079
XX DB 2546 GCGATAGAAAACAAATATAGCGGCAAACTAGGATTAATTAATCGCGCGGTGTCATCT 2605
XX
XX QY 3080 ATGTTACTAGATCGAAC-----TCAGGSCATGGGATCCGCGCGCATGC 3124
XX DB 2606 ATGTTACTAGATCANNNGAATTCGATATCAAGCTTATCGATACCGCTCGACCTCGACGGG 2665
XX
XX QY 3125 GACGTGCGGCCCAATTCGCCCTATAGTGAATCGTATTAAC-----AATTCACTGGCGGTGTT 3181
XX DB 2666 GGCCCGGTATCCCAATTCGCCCTATAGTGAATCGTATTAACCGCGCTCACTGGCGGTGTT 2725
XX
XX QY 3182 TTCAACGTCGTGATCTGGGAAAACCTGGCGGTATCCCAACTTAATTCGCTTGCAGCACAT 3241
XX DB 2726 TTCAACGTCGTGATCTGGGAAAACCTGGCGGTATCCCAACTTAATTCGCTTGCAGCACAT 2785
XX
XX QY 3242 CCCCTTTTCGCGAGTGGCGTAATAGCGAAGAGCGCCGCAACCGATCGCCCTTCCCAACAG 3301
XX DB 2786 CCCCTTTTCGCGAGTGGCGTAATAGCGAAGAGCGCCGCAACCGATCGCCCTTCCCAACAG 2845
XX
XX QY 3302 TTGCGGAGCCGTGAATGGCGAAT-GGACGCGCCCTGTAGCGCGCATTAAGCGCGCGGGT 3360
XX DB 2846 TTGCGGAGCCGTGAATGGCGAATGGACGCGCCCTGTAGCGCGCATTAAGCGCGCGGGT 2905

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Db 3931 |||||CGCTTGATCGTTGGGAAACCGAGCTCAATGAAGCCATACAAACGACGAGCGTGACACC 3990
Qy 4501 ACATGCCCTGACGATGGCAACAAGCTTCGCGCAAACTATTAACTCGCGAACTACTTACT 4560
Db 3991 ACATGCCCTGACGATGGCAACAAGCTTCGCGCAAACTATTAACTCGCGAACTACTTACT 4950
Qy 4561 CTAGCTTCCCGGCAACAATTAATAGACTGAGAGCGGATAAAGTTGACGACCACTT 4620
Db 4051 CTAGCTTCCCGGCAACAATTAATAGACTGAGAGCGGATAAAGTTGACGACCACTT 4110
Qy 4621 CTGCGCTCGGCCCTTCGCGTGGCTGGTTATTGCTGATAAATCTGGAGCCGCTGAGCGT 4680
Db 4111 CTGCGCTCGGCCCTTCGCGTGGCTGGTTATTGCTGATAAATCTGGAGCCGCTGAGCGT 4170
Qy 4681 GGGTCTCGCGGTATCATTGACGACCTGGGCGCAGATGGTAAGCCCTCCCGTATCGTAGTT 4740
Db 4171 GGGTCTCGCGGTATCATTGACGACCTGGGCGCAGATGGTAAGCCCTCCCGTATCGTAGTT 4230
Qy 4741 ATCTACACGACGGGAGTCAAGCAACTATGATGAACGAAATAGACAGATCGCTGAGATA 4800
Db 4231 ATCTACACGACGGGAGTCAAGCAACTATGATGAACGAAATAGACAGATCGCTGAGATA 4290
Qy 4801 GGTGCTCCTGATTAAGATTTGGTAACTGTGACACCAAGTTTACTCATATATATTAG 4860
Db 4291 GGTGCTCCTGATTAAGATTTGGTAACTGTGACACCAAGTTTACTCATATATATTAG 4350
Qy 4861 ATTGATTTAAACCTTCACTTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTTGTGATAAT 4920
Db 4351 ATTGATTTAAACCTTCACTTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTTGTGATAAT 4410
Qy 4921 CTCATGACCAAAATPCCCTTAACTGAGTGTTCCTTCCACTGAGCGTCAGACCCCGTAGAA 4980
Db 4411 CTCATGACCAAAATPCCCTTAACTGAGTGTTCCTTCCACTGAGCGTCAGACCCCGTAGAA 4470
Qy 4981 AAGATCAAGAGATCTTCTGAGATCCTTTTCTGCGGTAACTCTGCTGCTGCAACA 5040
Db 4471 AAGATCAAGAGATCTTCTGAGATCCTTTTCTGCGGTAACTCTGCTGCTGCAACA 4530
Qy 5041 AAAAAACACCGCTTACAGCGGTGTTTGTTCGCGATCAAGAGCTACCAACTCTTTT 5100
Db 4531 AAAAAACACCGCTTACAGCGGTGTTTGTTCGCGATCAAGAGCTACCAACTCTTTT 4590
Qy 5101 CCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAAATCTGCTTCTAGTGTAGCCG 5160
Db 4591 CCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAAATCTGCTTCTAGTGTAGCCG 4650
Qy 5161 TAGTTAGCCACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCTGCTCTAATC 5220
Db 4651 TAGTTAGCCACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCTGCTCTAATC 4710
Qy 5221 CTGTTACAGTGGCTGCTGCAGTGGCGATAAGTCTGTCTTACCGGGTTGGACTCAAGA 5280
Db 4711 CTGTTACAGTGGCTGCTGCAGTGGCGATAAGTCTGTCTTACCGGGTTGGACTCAAGA 4770
Qy 5281 CGATAGTTACGGATAAGGCGACGCGTGGGCTGAAACGGGGGTTTCGTGACACAGCCC 5340
Db 4771 CGATAGTTACGGATAAGGCGACGCGTGGGCTGAAACGGGGGTTTCGTGACACAGCCC 4830
Qy 5341 AGCTTGGAGCGAAGCACTACCGAAGTACCTACAGCTGAGCTGATGAGAACG 5400
Db 4831 AGCTTGGAGCGAAGCACTACCGAAGTACCTACAGCTGAGCTGATGAGAACG 4890
Qy 5401 GCCACGCTTCCGGAAGGAGAAAGCGGACAGAGTATCGGTAAAGCGGAGGCTCGGAACA 5460
Db 4891 GCCACGCTTCCGGAAGGAGAAAGCGGACAGAGTATCGGTAAAGCGGAGGCTCGGAACA 4950
Qy 5461 GGAGAGCGACAGAGGAGCTTCCAGGGGAAACGCCCTGGTATCTTTATAGTCTGTGCGG 5520
Db 4951 GGAGAGCGACAGAGGAGCTTCCAGGGGAAACGCCCTGGTATCTTTATAGTCTGTGCGG 5010
Qy 5521 TTTTCGCCACCTCTGACTTGAAGCTGATTTTGTGATGCTCGTCAGGGGGCGGAGCTA 5580
|||||

Db 5011 TTTTCGCCACCTCTGACTTGGAGCGTCGATTTTTGTGATGCTGTCAGGGGGCGGAGCCTA 5070
Qy 5581 TGGAAAAACGCCAGCAACCGCGCTTTTACGGTTCCTGGCCTTTTCTGGCCTTTTGTCT 5640
Db 5071 TGGAAAAACGCCAGCAACCGCGCTTTTACGGTTCCTGGCCTTTTGTCTGGCCTTT 5130
Qy 5641 CACATGTTCTTCTCCTCGTTATCCCTGATCTCTGTGATAACCGTATTACCGCTTTGAG 5700
Db 5131 CACATGTTCTTCTCCTCGTTATCCCTGATCTCTGTGATAACCGTATTACCGCTTTGAG 5190
Qy 5701 TGAGCTGTATACCGCTCGCGCAGCCGAAACGACGAGCGAGTCAGTGACGAGGAA 5760
Db 5191 TGAGCTGTATACCGCTCGCGCAGCCGAAACGACGAGCGAGTCAGTGACGAGGAA 5250
Qy 5761 GCGGAAGAGCGCCCAATACGAAACCGCTCTCCCGCGCTTCCCGCGCTTCCATTAATGC 5820
Db 5251 GCGGAAGAGCGCCCAATACGAAACCGCTCTCCCGCGCTTCCCGCGCTTCCATTAATGC 5310
Qy 5821 AG 5822
Db 5311 AG 5312
RESULT 3
AAH25896/c
ID AAH25896 standard; DNA; 4229 BP.
XX
AC AAH25896;
XX
DT 24-AUG-2001 (first entry)
XX
DE Genetic information stability related oligonucleotide #5.
XX
KW Genetic information stability measurement; drug resistance; ds.
XX
OS Synthetic.
XX
PN JP2001087000-A.
XX
PD 03-APR-2001.
XX
PF 17-SEP-1999; 99JP-00264320.
XX
PR 17-SEP-1999; 99JP-00264320.
XX
PA (SENT-) SENTAN KAGAKU GIJUTSU INCUBATION CENT KK.
XX
DR WPI; 2001-360322/38.
XX
PT Measurement of stability of genetic information in an animal cell,
PT comprises introducing a vector having a gene resistant to a first drug
PT and a gene sensitive to a second drug, to an animal cell.
XX
PS Disclosure; Page 8-9; 12pp; Japanese.
XX
CC The present invention describes a method for the measurement of stability
CC of genetic information in an animal cell in which a vector having a gene
CC resistant to a first drug and a gene sensitive to a second drug is
CC introduced into the animal cell. This can be used for the measurement of
CC stability of genetic information in an animal cell. The present sequence
CC is an oligonucleotide used in the exemplification of the invention
XX
SQ Sequence 4229 BP; 1108 A; 1004 C; 1036 G; 1081 T; 0 U; 0 Other;
Query Match 46.1%; Score 2686; DB 4; Length 4229;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2686; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3137 AATTTCGCCCTATAGTGTGATGATTAACAATTCACCTGCGCGCTGTTTACACGCTGTGAC 3196
Db 3157 AATTTCGCCCTATAGTGTGATGATTAACAATTCACCTGCGCGCTGTTTACACGCTGTGAC 3098
Qy 3197 TGGGAAACCCCTGCGGTATACCAACTTAATCGCTTCAGCACATCCCCCTTCCGCCAGC 3256

||||| 3097 TGGGAAACCTTGGGTTACCCAACTTAATCGCTTGACGACATCCGCCCTTCCGACG 3038
||||| 3257 TGGCGTAATAGGAAGAGCGCGCACCAGATCGCCCTTCCCAACAGTTGCGAGCCTGAAT 3316
||||| 3037 TGGCGTAATAGGAAGAGCGCGCACCAGATCGCCCTTCCCAACAGTTGCGAGCCTGAAT 2978
||||| 3317 GCGGAATCGAGCGCCCTGTAGCGCGCATTAAGCGCGCGCGGGTGTGTGTTAGCGCA 3376
||||| 2977 GCGGAATCGAGCGCGCCCTGTAGCGCGCATTAAGCGCGCGCGGGTGTGTGTTAGCGCA 2918
||||| 3377 GCGTACCGCTACACTTGGCAGCGCCCTAGCGCCGCTCTTTCGCTTTCTTCCCTTCT 3436
||||| 2917 GCGTACCGCTACACTTGGCAGCGCCCTAGCGCCGCTCTTTCGCTTTCTTCCCTTCT 2858
||||| 3437 TCTCTGCCACGTTTCCCGGCTTTCGCGTCAAGCTCTAAATCGGGGCTCCCTTTAGGGT 3496
||||| 2857 TCTCTGCCACGTTTCCCGGCTTTCGCGTCAAGCTCTAAATCGGGGCTCCCTTTAGGGT 2798
||||| 3497 TCCGATTTAGAGCTTACCGGCACCTCGACCGCAAAACTTGAATTTGGGTGATGTTTAC 3556
||||| 2797 TCCGATTTAGAGCTTACCGGCACCTCGACCGCAAAACTTGAATTTGGGTGATGTTTAC 2738
||||| 3557 GTAGTGGCCATCGCCCTGATAGCGGTTTTTGGCCCTTTGACGTTGGAGTCCACGTTCT 3616
||||| 2737 GTAGTGGCCATCGCCCTGATAGCGGTTTTTGGCCCTTTGACGTTGGAGTCCACGTTCT 2678
||||| 3617 TTAATAGTGAATCTTTGTTTCAAACTGGAACAACACTCAACCCCTATCTCGGCTATTCTT 3676
||||| 2677 TTAATAGTGAATCTTTGTTTCAAACTGGAACAACACTCAACCCCTATCTCGGCTATTCTT 2618
||||| 3677 TTGATTTAAGGATTTTGGGATTTTGGGCTATTGGTAAATGAGCTGATTTAAC 3736
||||| 2617 TTGATTTAAGGATTTTGGGATTTTGGGCTATTGGTAAATGAGCTGATTTAAC 2558
||||| 3737 AAATATTTAACCGGAATTTTAAACAAATATTAACGTTTACAAATTTGCGCTGATCGGTAT 3796
||||| 2557 AAATATTTAACCGGAATTTTAAACAAATATTAACGTTTACAAATTTGCGCTGATCGGTAT 2498
||||| 3797 TTTCTCTTACGATCTGTGCGGTATTTCAACCGCATACAGGTGGCACTTTTGGGGAA 3856
||||| 2497 TTTCTCTTACGATCTGTGCGGTATTTCAACCGCATACAGGTGGCACTTTTGGGGAA 2438
||||| 3857 ATGTGCGGGAACCCCTATTGTTTATTTTCTAAATACATTCAAATATGATCGGCTCA 3916
||||| 2437 ATGTGCGGGAACCCCTATTGTTTATTTTCTAAATACATTCAAATATGATCGGCTCA 2378
||||| 3917 TGAGACAATAACCCCTGATAAATGCTTCAATAATTTGAAAAGGAAGATGATGATTC 3976
||||| 2377 TGAGACAATAACCCCTGATAAATGCTTCAATAATTTGAAAAGGAAGATGATGATTC 2318
||||| 3977 AACATTTCCGTGTCGCCCTTATCCCTTTTGGGCAATTTTGCTTCCCTTTTGCTC 4036
||||| 2317 AACATTTCCGTGTCGCCCTTATCCCTTTTGGGCAATTTTGCTTCCCTTTTGCTC 2258
||||| 4037 ACCAGAAACCTGGTGAAGTAAAGTGTGAGATCAGTTGGGTGACAGTGGGT 4096
||||| 2257 ACCAGAAACCTGGTGAAGTAAAGTGTGAGATCAGTTGGGTGACAGTGGGT 2198
||||| 4097 ACATCGAATCGAATCTCAACAGCGTAAAGTCTTGAAGTCTTGGGCAATTTGCGCCCGGAAGACGTT 4156
||||| 2197 ACATCGAATCGAATCTCAACAGCGTAAAGTCTTGAAGTCTTGGGCAATTTGCGCCCGGAAGACGTT 2138
||||| 4157 TTCATGATGAGCACTTTTAAAGTCTGCTATGTTGGCGGATATTAATCCGCTATTGACG 4216
||||| 2137 TTCATGATGAGCACTTTTAAAGTCTGCTATGTTGGCGGATATTAATCCGCTATTGACG 2078
||||| 4217 CCGGCAAGAGCACTCGGTGCGCGCATACACTATTCTCAAGATGACTTGGTTGAGTACT 4276
||||| 2077 CCGGCAAGAGCACTCGGTGCGCGCATACACTATTCTCAAGATGACTTGGTTGAGTACT 2018
||||| 4277 CACAGTCACAGAAAGCATCTTACGATGTCATGACAGTAAAGATTAATGATGCTG 4336
|||||

2017 CACCAGTCACAGAAAGCATCTTACGATGGCATGACAGTAAGAGAAATATTCAGTGCTG 1958
4337 CCATAACCATGAGTAAACACTCGCGCAACTTACTTCTGCAACGATCGGAGACCGA 4396
1957 CCATAACCATGAGTAAACACTCGCGCAACTTACTTCTGCAACGATCGGAGACCGA 1898
4397 AGGAGCTAACCGCTTTTGTGACAACTGGGGGATCATGTAACTCGCTTGTGCTGG 4456
1897 AGGAGCTAACCGCTTTTGTGACAACTGGGGGATCATGTAACTCGCTTGTGCTGG 1838
4457 AACCGAGCTCAATGAAGCCATACCAACGAGCGGTGACACACGATGCTGTAGCAA 4516
1837 AACCGAGCTCAATGAAGCCATACCAACGAGCGGTGACACACGATGCTGTAGCAA 1778
4517 TGGCAACAACTGTGCGCAACTATTAATGCGCAACTACTTACTCTAGCTTCCCGCAAC 4576
1777 TGGCAACAACTGTGCGCAACTATTAATGCGCAACTACTTACTCTAGCTTCCCGCAAC 1718
4577 AATTAATAGACTGGATGGGCGGATAAAGTTGACGACCACTTCTGCGTCCGCCCTTC 4636
1717 AATTAATAGACTGGATGGGCGGATAAAGTTGACGACCACTTCTGCGTCCGCCCTTC 1658
4637 CCGCTGGCTGTTTATGCTGATAAATCTGAGCGCGTGAGCGTGGGTCTCGCGTATCA 4696
1657 CCGCTGGCTGTTTATGCTGATAAATCTGAGCGCGTGAGCGTGGGTCTCGCGTATCA 1598
4697 TTGAGCACTGGGCGAGATGATGAGCCCTCCGCTATCGTATCTTACTACGACGGGA 4756
1597 TTGAGCACTGGGCGAGATGATGAGCCCTCCGCTATCGTATCTTACTACGACGGGA 1538
4757 GTGAGCACTGGGCGAGATGATGAGCCCTCCGCTATCGTATCTTACTACGACGGGA 4816
1537 GTGAGCACTGGGCGAGATGATGAGCCCTCCGCTATCGTATCTTACTACGACGGGA 1478
4817 AGCATTTGTAATCTGTACAGCAAGTTTACTCATATATATTTAGATTGATTTAAACTTC 4876
1477 AGCATTTGTAATCTGTACAGCAAGTTTACTCATATATATTTAGATTGATTTAAACTTC 1418
4877 ATTTTAAATTTAAAGGATCTAGGTGAAGATCTTTTGTATATCTCATGACCAAAATCC 4936
1417 ATTTTAAATTTAAAGGATCTAGGTGAAGATCTTTTGTATATCTCATGACCAAAATCC 1358
4937 CTTAAGCTGAGTTTGGTTCACCTGAGCGTACAGCCCGTGAAGAAAGTCAAGATCTT 4996
1357 CTTAAGCTGAGTTTGGTTCACCTGAGCGTACAGCCCGTGAAGAAAGTCAAGATCTT 1298
4997 CTTGAGATCTCTTTTCTGCGCGTAACTCTGCTGTCGCAACCAAAACACCGCTAC 5056
1297 CTTGAGATCTCTTTTCTGCGCGTAACTCTGCTGTCGCAACCAAAACACCGCTAC 1238
5057 CAGCGTGGTGTGTTTGGCGGATCAAGAGCTACCAACTCTTTTCCGAAGTAACTGGCT 5116
1237 CAGCGTGGTGTGTTTGGCGGATCAAGAGCTACCAACTCTTTTCCGAAGTAACTGGCT 1178
5117 TCAGCAGCGCAGATACCAAACTGCTCTTAGTGTAGCCGCTAGTTAGCCACACT 5176
1177 TCAGCAGCGCAGATACCAAACTGCTCTTCTTAGTGTAGCCGCTAGTTAGCCACACT 1118
5177 TCAAGAACTCTGTAGCAGCGCTACATACCTGCTCTGCTAATCTGTTTACAGTGGCTG 5236
1117 TCAAGAACTCTGTAGCAGCGCTACATACCTGCTCTGCTAATCTGTTTACAGTGGCTG 1058
5237 CTGCGAGTGGCGATAAGTCTGCTTACCAGGTTGGACTCAAGACGATAGTTTACCGGATA 5296
1057 CTGCGAGTGGCGATAAGTCTGCTTACCAGGTTGGACTCAAGACGATAGTTTACCGGATA 998
5297 AGGCGCAGCGTGGGCTGAAACGGGGGTTGCTGCAACAGCCGAGCTTGGAGCAACGA 5356
997 AGGCGCAGCGTGGGCTGAAACGGGGGTTGCTGCAACAGCCGAGCTTGGAGCAACGA 938
5357 CTTACCGCACTGAGATACCTACAGCGTGGCTATGAGAAAGCGCCAGCTTCCCGAAG 5416
937 CTTACCGCACTGAGATACCTACAGCGTGGCTATGAGAAAGCGCCAGCTTCCCGAAG 878

QY 5417 GGAGAAAGCGGACAGTATCCGGTAAGCGGACAGGCTCGGAAACAGAGAGCGCACGAGGG 5476
DB 877 GGAGAAAGCGGACAGTATCCGGTAAGCGGACAGGCTCGGAAACAGAGAGCGCACGAGGG 818
QY 5477 AGCTTCAGGGGAAACCGCTGCTATCTTTATAGTCTCTGTCGGGTTTCGCCACTCTGAC 5536
DB 817 AGCTTCAGGGGAAACCGCTGCTATCTTTATAGTCTCTGTCGGGTTTCGCCACTCTGAC 758
QY 5537 TTGAGCGTCAATTTTGTGATGCTCTGTCAGGGGGGGGAGCCTATGGAAGAAACGCCAGCA 5596
DB 757 TTGAGCGTCAATTTTGTGATGCTCTGTCAGGGGGGGGAGCCTATGGAAGAAACGCCAGCA 698
QY 5597 ACGCGGCTTTTACGGTTCTCGGCTTTTGTGCTGGCCTTTTGTCTCATGCTTCTTCTG 5656
DB 697 ACGCGGCTTTTACGGTTCTCGGCTTTTGTGCTGGCCTTTTGTCTCATGCTTCTTCTG 638
QY 5657 CGTTATCCCTGATTTCTGCTGAATAACCGTATTAACCGCTTTTGTAGTGAGCTGATACCGCTC 5716
DB 637 CGTTATCCCTGATTTCTGCTGAATAACCGTATTAACCGCTTTTGTAGTGAGCTGATACCGCTC 578
QY 5717 GCCGACGCCGAACGACGAGCGGACGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAA 5776
DB 577 GCCGACGCCGAACGACGAGCGGACGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAA 518
QY 5777 TAGCMAAACCGCTCTCCCGCGGCTTGGCGGATTCAATTAATGCGAG 5822
DB 517 TAGCMAAACCGCTCTCCCGCGGCTTGGCGGATTCAATTAATGCGAG 472

RESULT 4

ABQ84197/c

ID ABQ84197 standard; DNA; 3448 BP.

AC ABQ84197;

XX

DT 19-FEB-2003 (first entry)

DE Vector pGEMTE1sh6 DNA SEQ ID NO:6.

XX

KW Hepatitis C virus; HCV; envelope protein; gene therapy; virucide;
KW antiinflammatory; gene therapy; vaccine; gene; ds.
XX

OS Hepatitis C virus.

OS Synthetic.

XX

PN WO200285932-A2.

XX

PD 31-OCT-2002.

XX

PF 24-APR-2002; 2002WO-BE000062.

XX

PR 24-APR-2001; 2001EP-00870088.

XX

PR 17-JUL-2001; 2001US-0305604P.

XX

PA (INNO-) INNOGENETICS NV.

XX

PI Sablon E, Van Broekhoven A, Bosman A, Depla E, Deschamps G;

XX

DR WPI; 2003-093095/08.

XX

PT New recombinant nucleic acids for expressing Hepatitis C virus (HCV)
PT envelope proteins in eukaryotic cells, comprising a sequence encoding a
PT protein having an avian lysozyme leader peptide joined to the HCV
PT envelope protein.
XX

PS Example 1; Page 165-167; 319pp; English.

XX

CC The present invention describes a recombinant nucleic acid (I) comprising
CC a nucleotide sequence encoding a protein having an avian lysozyme leader
CC peptide, or its functional equivalent, joined to a Hepatitis C virus
CC (HCV) envelope protein or its part. Also described: (1) a vector
CC comprising the recombinant nucleic acid; (2) a host cell comprising the

CC recombinant nucleic acid or the vector; and (3) a method for producing
CC HCV envelope protein or its part in a host cell, comprising transforming
CC the host cell with the recombinant nucleic acid or with the vector, where
CC the host cell is capable of expressing the protein cited above. (1) has
CC hepatotropic, virucide and antiinflammatory activities, and can be used
CC in gene therapy and vaccines. The recombinant nucleic acid is useful for
CC efficient expression of Hepatitis C virus envelope proteins in eukaryotic
CC cells, such as yeast cells. The HCV envelope proteins may be used as a
CC vaccine, or for incorporation into an immunoassay for the detection of
CC anti-HCV antibodies, and/or genotyping of HCV, for prognosing or
CC monitoring of HCV disease, or as a therapeutic agent. The method is used
CC for producing HCV envelope protein or its part in a host cell. ABQ84197
CC to ABQ84253 and ABP55528 to ABP55568 represent sequences used in the
CC exemplification of the present invention
XX

SQ Sequence 3448 BP; 862 A; 883 C; 879 G; 824 T; 0 U; 0 Other;

Query Match 46.1%; Score 2683.4; DB 7; Length 3448;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2693; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 3114 CGGCGCATCGGACGTCGGGCCCAATTGCGCCCTATAGTGAAGTCTATTACAATCACTGG 3173
DB 2985 CGGAGCATCGGACGTCGGGCCCAATTGCGCCCTATAGTGAAGTCTATTACAATCACTGG 2926
QY 3174 CGGTCGCTTTTACAACGTCGTGACTGGGAAACCCCTGCGCTTACCCAACTTAATGCGCTTG 3233
DB 2925 CGGTCGCTTTTACAACGTCGTGACTGGGAAACCCCTGCGCTTACCCAACTTAATGCGCTTG 2866
QY 3234 CAGCACATCCCTTTTCGCCAGCTGGCGTAATAGCGAAGGCCCGCGATCGCCCTT 3293
DB 2865 CAGCACATCCCTTTTCGCCAGCTGGCGTAATAGCGAAGGCCCGCGATCGCCCTT 2806
QY 3294 CCCAACAGTTGCGCAGCTCGAATGGCGAATGGCGCCCTGTAGCGGCGCATTAAGCGC 3353
DB 2805 CCCAACAGTTGCGCAGCTCGAATGGCGAATGGCGCCCTGTAGCGGCGCATTAAGCGC 2746
QY 3354 GCGCGGTGTGGTGTGTACGCGCAGCGGTGACCGCTTACCTTGCAGAGCGCCCTTAGCGCCGC 3413
DB 2745 GCGCGGTGTGGTGTGTACGCGCAGCGGTGACCGCTTACCTTGCAGAGCGCCCTTAGCGCCGC 2686
QY 3414 TCCTTTGCGCTTTCTTCCCTTTCCTTTTCGCGCAGCTTGGCGGCTTCCCGTCAAGCTCT 3473
DB 2685 TCCTTTGCGCTTTCTTCCCTTTCCTTTTCGCGCAGCTTGGCGGCTTCCCGTCAAGCTCT 2626
QY 3474 AAATCGGGGCTCCCTTTAGGGTTCCGATTTAGAGCTTTACGGCACCTCGACCGCAAAA 3533
DB 2625 AAATCGGGGCTCCCTTTAGGGTTCCGATTTAGAGCTTTACGGCACCTCGACCGCAAAA 2566
QY 3534 ACTTGATTTGGGTGAGGTTTCACTAGTGGGCCATCGCCCTGTATAGACGGTTTTTCGCC 3593
DB 2565 ACTTGATTTGGGTGAGGTTTCACTAGTGGGCCATCGCCCTGTATAGACGGTTTTTCGCC 2506
QY 3594 TTTGACGTTGGAGTCCACGTTCTTTATAGTGGACTCTGTCCAACTGGAAACAACACT 3653
DB 2505 TTTGACGTTGGAGTCCACGTTCTTTATAGTGGACTCTGTTCAAAACCTGGAAACAACACT 2446
QY 3654 CAACCCCTATCTCGGTCTAATCTTTGATTTATAGGGAATTTGCGGATTTTCGGCTATTG 3713
DB 2445 CAACCCCTATCTCGGTCTAATCTTTGATTTATAGGGAATTTGCGGATTTTCGGCTATTG 2386
QY 3714 GTTAAAAAATGAGCTGATTTTAAACAAATATTTTAAACGGAATTTTAAACAAATATTAAGCTT 3773
DB 2385 GTTAAAAAATGAGCTGATTTTAAACAAATATTTTAAACGGAATTTTAAACAAATATTAAGCTT 2326
QY 3774 TACAATTTCCGCTGATGGGTATTTTCTCTTACGCATCTGTGGGTATTTTACACCGCA 3833
DB 2325 TACAATTTCCGCTGATGGGTATTTTCTCTTACGCATCTGTGGGTATTTTACACCGCA 2266
QY 3834 TACAGGTGGCACTTTTCGGGGAATGTGCGGGAACCCCTATTGTTTATTTTCTAAAT 3893
DB 2265 TACAGGTGGCACTTTTCGGGGAATGTGCGGGAACCCCTATTGTTTATTTTCTAAAT 2206

3894 ACATTCAAATATGATTCGCTCATGACAAATAACCCGTGATAAATGCTTCAATAATATG 3953
|||||
2205 ACATTCAAATATGATTCGCTCATGACAAATAACCCGTGATAAATGCTTCAATAATATG 2146
|||||
3954 AAAAAGGAAGATGATGATGATTAACAAATTTCCGCTGTCGCCCTTATTCCTTTTGGCGG 4013
|||||
2145 AAAAAGGAAGATGATGATGATTAACAAATTTCCGCTGTCGCCCTTATTCCTTTTGGCGG 2086
|||||
4014 ATTTTGGCTTCCTGTTTTTGGCTCAACCAGAAAACGCTGGTGAAGTAAAGATGCTGAAGA 4073
|||||
2085 ATTTTGGCTTCCTGTTTTTGGCTCAACCAGAAAACGCTGGTGAAGTAAAGATGCTGAAGA 2026
|||||
4074 TCAGTTGGGTGACGAGTGGGTATCATCTGAACCTGATCTCAACAGCGGTGAAGTCTTTGA 4133
|||||
2025 TCAGTTGGGTGACGAGTGGGTATCATCTGAACCTGATCTCAACAGCGGTGAAGTCTTTGA 1966
|||||
4134 GAGTTTTGCGCCGGAAGAAAGCTTTTCCAATGATGAGCACTTTTAAAGTCTTCTGCTATGCG 4193
|||||
1965 GAGTTTTGCGCCGGAAGAAAGCTTTTCCAATGATGAGCACTTTTAAAGTCTTCTGCTATGCTCA 1906
|||||
4194 CGCGTATATATCCGTTATGACGCGCGGGAAGAGCACTCGGTGCGCGCATACACTATTC 4253
|||||
1905 TACACTATTTATCCGTTATGACGCGCGGGAAGAGCACTCGGTGCGCGCGGTATTC 1846
|||||
4254 TCAGATGACTTGGTTGAGTACTCACCAGTACACAGAAAAGCATCTTACGGATGCGCATGAC 4313
|||||
1845 TCAGATGACTTGGTTGAGTACTCACCAGTACACAGAAAAGCATCTTACGGATGCGCATGAC 1786
|||||
4314 AGTAAGAGAATTTAGCAGTGTGCTGCAATAACCATGAGTGATAACACTCGCGCCAACTTACT 4373
|||||
1785 AGTAAGAGAATTTAGCAGTGTGCTGCAATAACCATGAGTGATAACACTCGCGCCAACTTACT 1726
|||||
4374 TCTGCAACCATGAGGAGGACGGAAGAGCTTAAACGCTTTTTTGGCAACATGCGGGATCA 4433
|||||
1725 TCTGCAACCATGAGGAGGACGGAAGAGCTTAAACGCTTTTTTGGCAACATGCGGGATCA 1666
|||||
4434 TGTAACTCGCTTGTATCGTTGGGAACCGAGCTGAATGAAGCCATACCAACAGCAGAGCG 4493
|||||
1665 TGTAACTCGCTTGTATCGTTGGGAACCGAGCTGAATGAAGCCATACCAACAGCAGAGCG 1606
|||||
4494 TGACACCAAGATGCTCTAGCAATGGCAACAACTTGGCAAACTATTAACCTGCGAACT 4553
|||||
1605 TGACACCAAGATGCTCTAGCAATGGCAACAACTTGGCAAACTATTAACCTGCGAACT 1546
|||||
4554 ACTTACTAGCTTCCGCGCAACAAATTAATAGATGGATGAGCGGATGAAGTTGAGG 4613
|||||
1545 ACTTACTAGCTTCCGCGCAACAAATTAATAGATGGATGAGCGGATGAAGTTGAGG 1486
|||||
4614 ACCACTTCTCGCTCGGCCCTTCGCGCTGCTGCTGTTTATTGCTGATAAATCTGGAGCGG 4673
|||||
1485 ACCACTTCTCGCTCGGCCCTTCGCGCTGCTGCTGTTTATTGCTGATAAATCTGGAGCGG 1426
|||||
4674 TGAGCTGGGTCTCGCGGTATCATTTGAGCACTGGGGCCAGATGGTAAGCCCTCCCGTAT 4733
|||||
1425 TGAGCTGGGTCTCGCGGTATCATTTGAGCACTGGGGCCAGATGGTAAGCCCTCCCGTAT 1366
|||||
4734 CGTAGTTATCTACAGCGGGGAGTCAAGGACATATGATGAAGAAATAGACAGATGCG 4793
|||||
1365 CGTAGTTATCTACAGCGGGGAGTCAAGGACATATGATGAAGAAATAGACAGATGCG 1306
|||||
4794 TGAGATAGGTGCTCACTGATTAAGCATTTGTAATCTGACCAAGTTTACTCATATAT 4853
|||||
1305 TGAGATAGGTGCTCACTGATTAAGCATTTGTAATCTGACCAAGTTTACTCATATAT 1246
|||||
4854 ACTTTAGATTGATTTAAACCTTCAATTTTAAAGGATCTAGGTGAAGATCCTTTT 4913
|||||
1245 ACTTTAGATTGATTTAAACCTTCAATTTTAAAGGATCTAGGTGAAGATCCTTTT 1186
|||||
4914 TGATAATCTCATGACCAAAATCCCTTAACTGAGTTTTCGTTCCACTGAGCGTCAGACCC 4973
|||||
1185 TGATAATCTCATGACCAAAATCCCTTAACTGAGTTTTCGTTCCACTGAGCGTCAGACCC 1126
|||||
4974 CGTAGAAAAGATCAAGGATCTTCTTGAGATCCCTTTTCTGCGCGTAAATCTGCTGCTT 5033
|||||

Db 1125 CGTAGAAAAGATCAAGGATCTTCTTGAGATCCTTTTCTGCGCGTAAATCTGCTGCTT 1066
|||||
QY 5034 GCAAAACAAAAACCCCGCTACAGCGGTGTTTGTTCGCGGATCAAGAGCTACCAAC 5093
|||||
Db 1065 GCAAAACAAAAACCCCGCTACAGCGGTGTTTGTTCGCGGATCAAGAGCTACCAAC 1006
|||||
QY 5094 TCTTTTCCGAAGTAACTGGCTTCAGCAGCGCAGATACCAATACTGCTCTCTAGT 5153
|||||
Db 1005 TCTTTTCCGAAGTAACTGGCTTCAGCAGCGCAGATACCAATACTGCTCTCTAGT 946
|||||
QY 5154 GTAGCCGTAGTTAGGCCACCACCTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCT 5213
|||||
Db 945 GTAGCCGTAGTTAGGCCACCACCTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCT 886
|||||
QY 5214 GCTAATCTCTTACCAGTGGCTGCTGCAAGTGGCAATAAGTCTGTCTTACCGGGTTGGA 5273
|||||
Db 885 GCTAATCTCTTACCAGTGGCTGCTGCAAGTGGCAATAAGTCTGTCTTACCGGGTTGGA 826
|||||
QY 5274 CTCAGACGATAGTTACCAGTAAAGCGCAGCGTGGGCTGACGGGGGTTCTGTCAC 5333
|||||
Db 825 CTCAGACGATAGTTACCAGTAAAGCGCAGCGTGGGCTGACGGGGGTTCTGTCAC 766
|||||
QY 5334 ACAGCCAGCTTCGAGCGAAACGACCTACACCGAACTGAGATACCTACAGCGTGTGACTATG 5393
|||||
Db 765 ACAGCCAGCTTCGAGCGAAACGACCTACACCGAACTGAGATACCTACAGCGTGTGACTATG 706
|||||
QY 5394 AGAAGCGCCACGCTTCCGAAAGGAGGAGGACAGGATATCCGTTAGCGGCAGGGT 5453
|||||
Db 705 AGAAGCGCCACGCTTCCGAAAGGAGGAGGACAGGATATCCGTTAGCGGCAGGGT 646
|||||
QY 5454 CGAACAGGAGAGCGCAGGAGGCTTCCAGGGGAAACGCTGTATCTTTATAGTCC 5513
|||||
Db 645 CGAACAGGAGAGCGCAGGAGGCTTCCAGGGGAAACGCTGTATCTTTATAGTCC 586
|||||
QY 5514 TGTCTGGGTTTCGCCACCTCTGACTGAGCGTTCGATTTTGTGATGCTCTGTCAGGGGGCG 5573
|||||
Db 585 TGTCTGGGTTTCGCCACCTCTGACTGAGCGTTCGATTTTGTGATGCTCTGTCAGGGGGCG 526
|||||
QY 5574 GAGCTATGAAAAACGCCAGCAACGCGCTTTTACGTTCTCTGCGCTTTTCTGCTGCC 5633
|||||
Db 525 GAGCTATGAAAAACGCCAGCAACGCGCTTTTACGTTCTCTGCGCTTTTCTGCTGCC 466
|||||
QY 5634 TTTTGTCTCATGTTCTTCTCTGCTTATCCCTGATTTCTGTGATTAACCGTATTACCG 5693
|||||
Db 465 TTTTGTCTCATGTTCTTCTCTGCTTATCCCTGATTTCTGTGATTAACCGTATTACCG 406
|||||
QY 5694 CTTTGTAGTGAGCTGATACCGCTCGCCGAGCCGAAACGAGCGCAGCGAGTCAGTGAG 5753
|||||
Db 405 CTTTGTAGTGAGCTGATACCGCTCGCCGAGCCGAAACGAGCGCAGCGAGTCAGTGAG 346
|||||
QY 5754 CGAGGAAGCGAAGAGCGCCAAATACGCAACCGCTCTCTCCCGCGGTTGGCGGATTCA 5813
|||||
Db 345 CGAGGAAGCGAAGAGCGCCAAATACGCAACCGCTCTCTCCCGCGGTTGGCGGATTCA 286
|||||
QY 5814 TTAATGCGAG 5822
|||||
Db 285 TTAATGCGAG 277
|||||

RESULT 5

AAD50589/c

ID AAD50589 standard; DNA; 3448 BP.

XX AAD50589;

XX AC
XX XX
DT 24-MAR-2003 (first entry)

XX pGEMTE1sh6 vector DNA.

XX Hepatitis C virus; HCV; envelope protein; virucide; immunostimulant;
KW immune response; T-cell; therapy; infection; pharmaceutical; vaccine;
KW gene; ds.

XX OS Unidentified.
XX PN WO200286101-A2.
XX PD 31-OCT-2002.
XX PF 24-APR-2002; 2002WO-BE000064.
XX PR 24-APR-2001; 2001EP-00870088.
XX PR 17-JUL-2001; 2001US-0305604P.
XX PA (INNO-) INNOGENETICS NV.
XX PI Depla E, Bosman A, Deschamps G, Sablon E, Suckow M, Samson I;
XX PI Verheyden G;
XX DR WPI; 2003-103409/09.
XX CC The invention relates to Hepatitis C virus (HCV) envelope protein with N-glycosylation site(s). The HCV envelope protein, or the pharmaceutical composition comprising the envelope protein, is useful as a medicament or a vaccine, particularly for inducing a HCV-specific immune response, inducing HCV-specific antibodies or inducing a T-cell function in a mammal. The protein is particularly useful for preventing, treating or diagnosing HCV infection. It is also useful for detecting the presence of anti-HCV antibodies in a sample. The present sequence is a vector DNA used in the exemplification of the invention
XX SQ Sequence 3448 BP; 862 A; 883 C; 879 G; 824 T; 0 U; 0 Other;
Query Match 46.1%; Score 2683.4; DB 7; Length 3448;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2693; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 3114 CGCGCGATCGACGTGCGGCCCAATTCGCCCTATAGTAGTGCATTAACAATCACTGG 3173
DB 2985 CGGGAGCATCGACGTGCGGCCCAATTCGCCCTATAGTAGTGCATTAACAATCACTGG 2926
QY 3174 CCCTCGTTTTACACGTGCTGCGGAAACCTCGCGTTACCCAACTTAATCGCCTTG 3233
DB 2925 CCCTCGTTTTACACGTGCTGCGGAAACCTCGCGTTACCCAACTTAATCGCCTTG 2866
QY 3234 CAGCACATCCCTTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGACCGATCGCCCTT 3293
DB 2865 CAGCACATCCCTTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGACCGATCGCCCTT 2806
QY 3294 CCCAACAGTTGCGAGCTGAATGGCGAATGACGCGCCCTGTAGCGGCGCATTAAGCGC 3353
DB 2805 CCCAACAGTTGCGAGCTGAATGGCGAATGACGCGCCCTGTAGCGGCGCATTAAGCGC 2746
QY 3354 GCGGGTGTGGTTACGCGAGCTGACCGCTACATGTCGAGCGCCCTAGCGCCCGC 3413
DB 2745 GCGGGTGTGGTTACGCGAGCTGACCGCTACATGTCGAGCGCCCTAGCGCCCGC 2686
QY 3414 TCCTTTTCGCTTTCTCCCTTCCCTTTTCGCCAGCTTCGCCGCTTTCCCGCTCAAGCTCT 3473
DB 2685 TCCTTTTCGCTTTCTCCCTTCCCTTTTCGCCAGCTTCGCCGCTTTCCCGCTCAAGCTCT 2626
QY 3474 AAATCGGGGCTCCCTTTAGGGTTCCGATTAGAGCTTTACGCGACCTGACCGCAAAA 3533
DB 2625 AAATCGGGGCTCCCTTTAGGGTTCCGATTAGAGCTTTACGCGACCTGACCGCAAAA 2566
QY 3534 ACTTGATTTGGGTGATGTTACGTAGTGGGCCATCGCCCTGATAGACGCTTTTCGCC 3593
DB 2565 ACTTGATTTGGGTGATGTTACGTAGTGGGCCATCGCCCTGATAGACGCTTTTCGCC 2506

QY 3594 TTTGAGCTTGGAGTCCACGTTCTTTAATAGTGACTCTTGTTCCAAACCTGGAACCACT 3653
DB 2505 TTTGAGCTTGGAGTCCACGTTCTTTAATAGTGACTCTTGTTCCAAACCTGGAACCACT 2446
QY 3654 CAACCCCTATCTCGGTCTATCTTTTGTATTAAGGGAATTTGCGGATTTTCGGCTATTG 3713
DB 2445 CAACCCCTATCTCGGTCTATCTTTTGTATTAAGGGAATTTGCGGATTTTCGGCTATTG 2386
QY 3714 GTTAAAAAATGAGCTGATTTTAAACAATATTTAACGCGAATTTTAAACAAAATATAAGCTT 3773
DB 2385 GTTAAAAAATGAGCTGATTTTAAACAATATTTAACGCGAATTTTAAACAAAATATAAGCTT 2326
QY 3774 TACAATTTCCGCTGATCGGCTATTTTCTCCTTACGCACTCTGCGGTATTTTCACACGCA 3833
DB 2325 TACAATTTCCGCTGATCGGCTATTTTCTCCTTACGCACTCTGCGGTATTTTCACACGCA 2266
QY 3834 TACAGTGGGACATTTTCGGGGAAATGTGCGGAAACCCCTATTTGTTTATTTTCTAAAT 3893
DB 2265 TACAGTGGGACATTTTCGGGGAAATGTGCGGAAACCCCTATTTGTTTATTTTCTAAAT 2206
QY 3894 ACATTTCAAAATATGATCCGCTCATGAGACAAATAACCTTGATAAATGCTTCAATAAATTTG 3953
DB 2205 ACATTTCAAAATATGATCCGCTCATGAGACAAATAACCTTGATAAATGCTTCAATAAATTTG 2146
QY 3954 AAAAAAGGAAAGATGAGTATTCAACATTTCCGTGCGCCCTTATTTCCCTTTTTCGCGC 4013
DB 2145 AAAAAAGGAAAGATGAGTATTCAACATTTCCGTGCGCCCTTATTTCCCTTTTTCGCGC 2086
QY 4014 ATTTTCCTTCTCTGTTTTTGTCTACCCAGAAACGCTGGTGAAGTAAGATGCTGAAGA 4073
DB 2085 ATTTTCCTTCTCTGTTTTTGTCTACCCAGAAACGCTGGTGAAGTAAGATGCTGAAGA 2026
QY 4074 TCAGTTGGGTGACGAGTGGGTTTACATCGAATCTCAACAGCGGTGAAGATCTCTTGA 4133
DB 2025 TCAGTTGGGTGACGAGTGGGTTTACATCGAATCTCAACAGCGGTGAAGATCTCTTGA 1966
QY 4134 GAGTTTTTCGCCCGAAGAACGTTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTTG 4193
DB 1965 GAGTTTTTCGCCCGAAGAACGTTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTTCA 1906
QY 4194 CGCGGTATTTATCCGTTATTTGACGCGGGCAAGAGCAATCGGTCGCGCGCATACATATTTC 4253
DB 1905 TACACTATTTATCCGTTATTTGACGCGGGCAAGAGCAACTCGGTCGCGCGCGGTATTC 1846
QY 4254 TCAGATGACTTGGTTGAGTACTCACAGTTCACAGAAAAGCATCTTTACGATGGCATGAC 4313
DB 1845 TCAGATGACTTGGTTGAGTACTCACAGTTCACAGAAAAGCATCTTTACGATGGCATGAC 1786
QY 4314 AGTAAGAGAAATTATGAGTGTCTGCCATAACCATGAGTGATAACACTCGCGCCCAACTTACT 4373
DB 1785 AGTAAGAGAAATTATGAGTGTCTGCCATAACCATGAGTGATAACACTCGCGCCCAACTTACT 1726
QY 4374 TCTGACAAAGATCGGAGGACGAGGAGCTTAACCGCTTTTTCGACAACTATGGGGATCA 4433
DB 1725 TCTGACAAAGATCGGAGGACGAGGAGCTTAACCGCTTTTTCGACAACTATGGGGATCA 1666
QY 4434 TGTAACCTCGCTTTGATCGTTGGAAACCGGAGCTGAATGAAGCCATACCAACCGCAGCG 4493
DB 1665 TGTAACCTCGCTTTGATCGTTGGAAACCGGAGCTGAATGAAGCCATACCAACCGCAGCG 1606
QY 4494 TGAACACAGATGCTGTAGCAATGGCAACAAAGTTTCGCGCAACTTAACTGCGCAACT 4553
DB 1605 TGAACACAGATGCTGTAGCAATGGCAACAAAGTTTCGCGCAACTTAACTGCGCAACT 1546
QY 4554 ACTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGAGGCGGATTAAGTTTCGAG 4613
DB 1545 ACTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGAGGCGGATTAAGTTTCGAG 1486
QY 4614 ACCACTTCTCGCTCGGCCCTTCCGGCTGGCTGTTTATTTGCTGATAAATCTCGAGCCGG 4673
DB 1485 ACCACTTCTCGCTCGGCCCTTCCGGCTGGCTGTTTATTTGCTGATAAATCTCGAGCCGG 1426

QY 4674 TGACGCTGGGTCTCGCGGTATCATTTGACGACCTGGGGCCAGATGGTAAAGCCCTCCCGTAT 4733
DB 1425 TGACGCTGGGTCTCGCGGTATCATTTGACGACCTGGGGCCAGATGGTAAAGCCCTCCCGTAT 1366
QY 4734 CGTAGTTATCTACACGACGGGAGTGCAGCACTATGGATGAACGAAATAGACAGATCGC 4793
DB 1365 CGTAGTTATCTACACGACGGGAGTGCAGCACTATGGATGAACGAAATAGACAGATCGC 1306
QY 4794 TGAGATAGTGGCTCACTGATTAAGCATTTGTAAGTGTGACACCAAGTTTACTATATAT 4853
DB 1305 TGAGATAGTGGCTCACTGATTAAGCATTTGTAAGTGTGACACCAAGTTTACTATATAT 1246
QY 4854 ACTTTAGATTGATTTAAACTTCACTTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTTT 4913
DB 1245 ACTTTAGATTGATTTAAACTTCACTTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTTT 1186
QY 4914 TGATAATCTCATGACCAAAATCCCTTAACTGAGTGTTCCTCCACTGAGCGTCAGACCC 4973
DB 1185 TGATAATCTCATGACCAAAATCCCTTAACTGAGTGTTCCTCCACTGAGCGTCAGACCC 1126
QY 4974 CGTAGAAGATCAAGGATCTCTTCTGAGATCCCTTTTCTGCGCGTAAATCTGCTGCTT 5033
DB 1125 CGTAGAAGATCAAGGATCTCTTCTGAGATCCCTTTTCTGCGCGTAAATCTGCTGCTT 1066
QY 5034 GCAACCAAAAAACACCGCTACAGCGGTGCTTTTGTTCGCGGATCAAGAGCTACCAAC 5093
DB 1065 GCAACCAAAAAACACCGCTACAGCGGTGCTTTTGTTCGCGGATCAAGAGCTACCAAC 1006
QY 5094 TCTTTTCCGAAGTAACTGGCTTTCAGCAGACGCGAGATACCAATATCTGCTCTTCTAGT 5153
DB 1005 TCTTTTCCGAAGTAACTGGCTTTCAGCAGACGCGAGATACCAATATCTGCTCTTCTAGT 946
QY 5154 GTAGCCGTAGTTAGCCACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTGCTCT 5213
DB 945 GTAGCCGTAGTTAGCCACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTGCTCT 886
QY 5214 GCTAATCTGTTACAGTGGCTGCTGCAGTGGCGATAAGTCGTCTTACCGGTTTGA 5273
DB 885 GCTAATCTGTTACAGTGGCTGCTGCAGTGGCGATAAGTCGTCTTACCGGTTTGA 826
QY 5274 CTCGAAGCATAGTTACCGGATAAGGCGCAGCGTTCGGGCTGAACGGGGGTTCTGTCAC 5333
DB 825 CTCGAAGCATAGTTACCGGATAAGGCGCAGCGTTCGGGCTGAACGGGGGTTCTGTCAC 766
QY 5334 ACAGCCAGCTTGGAGGAGCACTACACCGAATGAGATACCTACAGGTGAGCTATG 5393
DB 765 ACAGCCAGCTTGGAGGAGCACTACACCGAATGAGATACCTACAGGTGAGCTATG 706
QY 5394 AGAAGCGCCACGCTTCCGGAAGGAGAAAGCGGACAGGTATCCGGTAAAGCGGAGGTT 5453
DB 705 AGAAGCGCCACGCTTCCGGAAGGAGAAAGCGGACAGGTATCCGGTAAAGCGGAGGTT 646
QY 5454 CGGAACAGGAGAGCGCAGGAGCTTCCAGGGGAGAAACCGCTGATCTTTATAGTCC 5513
DB 645 CGGAACAGGAGAGCGCAGGAGCTTCCAGGGGAGAAACCGCTGATCTTTATAGTCC 586
QY 5514 TGTCGGGTTTCCGCACTCTGACTGAGCTGCAATTTTGTGATGCTGCTGAGGGGGCG 5573
DB 585 TGTCGGGTTTCCGCACTCTGACTGAGCTGCAATTTTGTGATGCTGCTGAGGGGGCG 526
QY 5574 GAGCCTATGAAAAACGCGCAGCAACGCGGCTTTTACGGTTCTGCGGCTTTTCTGCGC 5633
DB 525 GAGCCTATGAAAAACGCGCAGCAACGCGGCTTTTACGGTTCTGCGGCTTTTCTGCGC 466
QY 5634 TTTTGTCTCACAATGTTCTTCTGCGTTATCCCTGATTTCTGTGGATAACCGTATTACCGC 5693
DB 465 TTTTGTCTCACAATGTTCTTCTGCGTTATCCCTGATTTCTGTGGATAACCGTATTACCGC 406
QY 5694 CTTTGTAGTGAAGTATACCGCTCGCGGAGCGGAAACGAGCGGAGCGAGTCAAGTGA 5753
DB 405 CTTTGTAGTGAAGTATACCGCTCGCGGAGCGGAAACGAGCGGAGCGAGTCAAGTGA 346
QY 5754 CGAGGAAGCGGAAGAGCGCCCAATACGCAACCGCCCTCTCCCGCGGCTTGGCGGATTC 5813

DB 345 CGAGGAGCGGAAGAGCGCCCAATACGCAACCGCCCTCTCCCGCGGCTTGGCGGATTC 286
QY 5814 TTAATGCAG 5822
DB 285 TTAATGCAG 277
RESULT 6
ABT14439/c
ID ABT14439 standard; DNA; 3448 BP.
XX AC ABT14439;
XX 18-FEB-2003 (first entry)
XX HCV envelope protein related vector DNA sequence SEQ ID No 6.
XX Hepatotropic; Hepatitis C Virus; HCV virus; HCV envelope protein; HCV E1;
XX HCV E2; vaccine; Hansecula polymorpha; viral envelope protein;
XX glycosylated; ds.
XX OS Unidentified.
XX WO200286100-A2.
XX 31-OCT-2002.
XX 24-APR-2002; 2002WO-BE000063.
XX 24-APR-2001; 2001EP-00870088.
XX 17-JUL-2001; 2001US-0305604P.
XX (INNO-) INNOGENETICS NV.
XX Bosman A, Depla E, Deschamps G, Sablon E, Samson I;
XX Van Broekhoven A, Haelewyn J;
XX WPI; 2003-093130/08.
XX New Hepatitis C Virus (HCV) virus-like particle formed of an HCV envelope
XX protein or its part, useful for treating or preventing HCV infection.
XX Example 7; Page 158-160; 296pp; English.
XX The invention relates to a Hepatitis C Virus (HCV) virus-like particle
XX formed of an HCV envelope protein or its part, where the cysteines are
XX chemically and reversibly modified. The HCV E1 and/or HCV E2 proteins are
XX useful for the manufacture of a vaccine or medicament against HCV
XX infection or for preparing a diagnostic kit. The Hansecula polymorpha is
XX useful for the expression of viral envelope proteins that become
XX glycosylated upon expression in this yeast species. This polynucleotide
XX sequence represents the DNA of a vector relating to the HCV envelope
XX proteins of the invention
XX
XX Sequence 3448 BP; 861 A; 882 C; 879 G; 823 T; 0 U; 3 Other;
Query Match 46.0%; Score 2680.4; DB 7; Length 3448;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2690; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 3114 CGGCGCATCGGACGTCGGGCCCAATTCGCCCTATAGTGTGATTAACAATTCATG 3173
DB 2985 CGGAGCATCGGACGTCGGGCCCAATTCGCCCTATAGTGTGATTAACAATTCATG 2926
QY 3174 CCGTCGTTTACACGTCGTGACTGGGAAACCTCGGTTACCAACTTAATCGCCTTG 3233
DB 2925 CCGTCGTTTACACGTCGTGACTGGGAAACCTCGGTTTACCAACTTAATCGCCTTG 2866
QY 3234 CAGCACATCCCTTTTCGCCAGCTGGCGTAAATAGCAAGAGCCCGACCGATCGCCTT 3293
DB 2865 CAGCACATCCCTTTTCGCCAGCTGGCGTAAATAGCAAGAGCCCGACCGATCGCCTT 2806

QY 3294 CCCAACAGTTGCGACGCTGAATGGCGAATGGACGCGCCCTGTAGCGGCCATTAAGCGC 3353
Db CCCAACAGTTGCGACGCTGAATGGCGAATGGACGCGCCCTGTAGCGGCCATTAAGCGC 2746
QY 3354 GCGGGTGTGGTGTACGGCAGCGTGACCGCTACATTGCCAGCGCCCTAGCGCCGC 3413
Db GCGGGTGTGGTGTACGGCAGCGTGACCGCTACATTGCCAGCGCCCTAGCGCCGC 2686
QY 3414 TCCCTTCGCTTCTTCCCTTCTTCGCGCAGTTCGCGCGCTTTCGCCGTCAAGCTCT 3473
Db TCCCTTCGCTTCTTCCCTTCTTCGCGCAGTTCGCGCGCTTTCGCCGTCAAGCTCT 2626
QY 3474 AAATCGGGGCTCCCTTTAGGGTTCCGATTTAGAGCTTTTACGGCACCTCGACCGCAAAA 3533
Db AAATCGGGGCTCCCTTTAGGGTTCCGATTTAGAGCTTTTACGGCACCTCGACCGCAAAA 2566
QY 3534 ACTTGATTTGGGTAGTGTTACGTAGTGGCCATCGCCCTGTAGACGGTTTTTCGCC 3593
Db ACTTGATTTGGGTAGTGTTACGTAGTGGCCATCGCCCTGTAGACGGTTTTTCGCC 2506
QY 3594 TTTGACGTTGGAGTCCACGTTCTTTAATAGTGACCTCTTGTCCAAACTGGAAACAACCT 3653
Db TTTGACGTTGGAGTCCACGTTCTTTAATAGTGACCTCTTGTCCAAACTGGAAACAACCT 2446
QY 3654 CAACCCCTATCTCGTCTATTTCTTTGATTTATAGGGATTTTCGGATTTTCGGCCTATTG 3713
Db CAACCCCTATCTCGTCTATTTCTTTGATTTATAGGGATTTTCGGATTTTCGGCCTATTG 2386
QY 3714 GTTAAAAATGAGCTGATTTTAAACAATTTTAAACGGGAATTTTAAACAATATTAAGT 3773
Db GTTAAAAATGAGCTGATTTTAAACAATTTTAAACGGGAATTTTAAACAATATTAAGT 2326
QY 3774 TACAATTTCCCTGATCGGCTATTTCTCTTACGCACTCTGCGGTATTTTACACCGCA 3833
Db TACAATTTCCCTGATCGGCTATTTCTCTTACGCACTCTGCGGTATTTTACACCGCA 2266
QY 3834 TACAGTGGCACTTTTCGGGAAATGTGCGGAAACCCCTATTGTTTATTTTCAAAT 3893
Db TACAGTGGCACTTTTCGGGAAATGTGCGGAAACCCCTATTGTTTATTTTCAAAT 2206
QY 3894 ACATTCAAATATGATTCGCTCATGACACAATTAACCTGATAATGCTTCAATAATATG 3953
Db ACATTCAAATATGATTCGCTCATGACACAATTAACCTGATAATGCTTCAATAATATG 2146
QY 3954 AAAAAGGAAGATGATGAGTATTCAAATTTCCGTGTGCGCCCTATTCCCTTTTTCGGC 4013
Db AAAAAGGAAGATGATGAGTATTCAAATTTCCGTGTGCGCCCTATTCCCTTTTTCGGC 2086
QY 4014 ATTTTGCCTTCCTGTTTTTGTCTACCCAGAAACGCTGGTGAAGTAAAGATGCTGAAGA 4073
Db ATTTTGCCTTCCTGTTTTTGTCTACCCAGAAACGCTGGTGAAGTAAAGATGCTGAAGA 2026
QY 4074 TCAGTTGGGTGACGAGTGGTTTACATCGAATCGATCTCAACAGCGGTAAAGTCCCTGA 4133
Db TCAGTTGGGTGACGAGTGGTTTACATCGAATCGATCTCAACAGCGGTAAAGTCCCTGA 1966
QY 4134 GAGTTTTTCGCCCGAAGAAAGCTTTTCAATGATGAGCACTTTTAAAGTTCTGCTATGCG 4193
Db GAGTTTTTCGCCCGAAGAAAGCTTTTCAATGATGAGCACTTTTAAAGTTCTGCTATGCG 1906
QY 4194 CGCGGTATTTATCCGTTATTCAGCGCGGCAAGAGCAACTCGGTGCGCGCATACACTATTC 4253
Db TACACTATTATCCGTTATTCAGCGCGGCAAGAGCAACTCGGTGCGCGCGGTATTC 1846
QY 4254 TCAGAAATGACTTGGTTCAGTACTCACAGTCAAGAAAGCACTTTACGGATGGCATGAC 4313
Db TCAGAAATGACTTGGTTCAGTACTCACAGTCAAGAAAGCACTTTACGGATGGCATGAC 1786
QY 4314 AGTAAGAGAAATTTATSCAGTGTGCGCAATCCATGAGTGATAACACTCGCGCCCACTTACT 4373
Db AGTAAGAGAAATTTATSCAGTGTGCGCAATCCATGAGTGATAACACTCGCGCCCACTTACT 1726
QY 4374 TCTGACAACGATTCGAGACCGAAGAGCTAAACGCTTTTTTGGCAACAATGGGGATCA 4433

Db 1725 TCTGACAAACGATCGAGGACCGAAGGAGCTTAACCGCTTTTTTGCACAAATGGGGATCA 1666
QY 4434 TGTAACTCGCTTGTATCGTTTGGGAAACCGGAGCTGMAATGAAGCCATACCAACGACGAGCG 4493
Db TGTAACTCGCTTGTATCGTTTGGGAAACCGGAGCTGMAATGAAGCCATACCAACGACGAGCG 1606
QY 4494 TGAACACACGATCGCTGTAGCAATGGCAACAAAGTTTGCACAAACTATTAATCTGGCGAACT 4553
Db TGAACACACGATCGCTGTAGCAATGGCAACAAAGTTTGCACAAACTATTAATCTGGCGAACT 1546
QY 4554 ACTTACTAGCTTCCGGCAACAATTAATAGACTGATGAGGAGCGGATTAAGTTGACGG 4613
Db ACTTACTAGCTTCCGGCAACAATTAATAGACTGATGAGGAGCGGATTAAGTTGACGG 1486
QY 4614 ACCACTTCTGCGCTCGGCCCTTCCGCTGCTGGTTTATTGCTGATAAAATCTCGAGCCGG 4673
Db ACCACTTCTGCGCTCGGCCCTTCCGCTGCTGGTTTATTGCTGATAAAATCTCGAGCCGG 1426
QY 4674 TGAGCGTGGGTCTCGCGGTATCAATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTAT 4733
Db TGAGCGTGGGTCTCGCGGTATCAATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTAT 1366
QY 4734 CGTAGTTATCTACAGCACGGGAGTCAAGCAACTATGGATGAACGAATAAGACAGATCGC 4793
Db CGTAGTTATCTACAGCACGGGAGTCAAGCAACTATGGATGAACGAATAAGACAGATCGC 1306
QY 4794 TGAGATAGGTGCTCTACTGATTAAGCACTTGGTAACCTGTAGACCAAGTTTACTCATATAT 4853
Db TGAGATAGGTGCTCTACTGATTAAGCACTTGGTAACCTGTAGACCAAGTTTACTCATATAT 1246
QY 4854 ACTTTAGATTGATTTAAAACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTT 4913
Db ACTTTAGATTGATTTAAAACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTT 1186
QY 4914 TGAATATCTCATGACCAAAATCCCTTAACTGAGTTTTCGTTCCACTGAGGCTCAGACCC 4973
Db TGAATATCTCATGACCAAAATCCCTTAACTGAGTTTTCGTTCCACTGAGGCTCAGACCC 1126
QY 4974 CGTAGAAAAGATCAAAAGGATCTTCTGAGATCCCTTTTTTCTGCGCGTAATCTGCTGCT 5033
Db CGNNNAAAAGATCAAAAGGATCTTCTGAGATCCCTTTTTTCTGCGCGTAATCTGCTGCT 1066
QY 5034 GCAAAACAAAAACCAACCGCTACAGCGGTGTTGTTTCCGGATCAAGAGTACCAAC 5093
Db GCAAAACAAAAACCAACCGCTACAGCGGTGTTGTTTCCGGATCAAGAGTACCAAC 1006
QY 5094 TCTTTTTCCGAAGGTAACTGGCTTCAGCAGCGCAGATACCAATACTCTCTCTAGT 5153
Db TCTTTTTCCGAAGGTAACTGGCTTCAGCAGCGCAGATACCAATACTCTCTCTCTAGT 946
QY 5154 GTAGCGGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCT 5213
Db GTAGCGGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCT 886
QY 5214 GCTAATCTCTTACCAAGTGGCTGCTGCGAGTGGCGATAAGTCGTGCTTACC GGTTGGA 5273
Db GCTAATCTCTTACCAAGTGGCTGCTGCGAGTGGCGATAAGTCGTGCTTACC GGTTGGA 826
QY 5274 CTCAAGACGATAGTTACCGGATTAAGCGCAGCGGTGCGGCTGAAACGGGGGTTCTGTCAC 5333
Db CTCAAGACGATAGTTACCGGATTAAGCGCAGCGGTGCGGCTGAAACGGGGGTTCTGTCAC 766
QY 5334 ACAGCCGAGCTTGGAGCGAAGCACTTACCCGAATGAGATACCTACAGCGTGAAGTATG 5393
Db ACAGCCGAGCTTGGAGCGAAGCACTTACCCGAATGAGATACCTACAGCGTGAAGTATG 706
QY 5394 AGAAAGCGCACGCTTCCCGAAGGAGAAAGCGGACAGGTATCCGCTAAGCGCAGGGT 5453
Db AGAAAGCGCACGCTTCCCGAAGGAGAAAGCGGACAGGTATCCGCTAAGCGCAGGGT 646
QY 5454 CGGACAGGAGCGCACGAGGAGCTTCCAGGGGAAACGCTGATCTTTTATAGTCC 5513

PT Novel construct for preventing embryogenesis in animals comprises native
PT promoter, blocking DNA which abrogates function of crucial gene and
PT genetic switch to regulate expression/repression of blocker/gene
PT knockout.
XX
PS
PS Example 8; Page 196-198; 24lpp; English.
XX
CC The invention relates to a construct which allows animals to be bred in
CC captivity but renders them infertile in the wild by allowing reversible
CC control over fertility and reproduction. The construct comprises a native
CC promoter, a blocking DNA sequence contoured for and designed to abrogate
CC a crucial gene's function or to cause its mis-expression, and a genetic
CC switch to regulate controlled expression/repression of the blocker/gene
CC knockout. The construct is useful for preventing embryogenesis or
CC gametogenesis in animals by stably transforming an animal cell with the
CC construct by microinjection, transfection or infection, where the
CC construct stably integrates into the genome by homologous recombination,
CC and implanting the cell into a host organism, where a whole animal
CC develops from the implanted cell. The present DNA sequence is plasmid
CC construct pHSP-GUS construct used for transfection of Pacific oysters.
CC The plasmid contains glucuronidase (GUS) gene under the control of
CC Drosophila heat shock promoter (dHSP)
XX
SQ Sequence 5919 BP; 1504 A; 1474 C; 1414 G; 1527 T; 0 U; 0 Other;
Query Match 46.0%; Score 2675.4; DB 4; Length 5919;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2676; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3146 TATAGTCAGTCGTATTACAAATTCACGCGCGTCGTTTACAACTCGTACTGGGAAAC 3205
DB TATAGTCAGTCGTATTACAAATTCACGCGCGTCGTTTACAACTCGTACTGGGAAAC 5860
QY 3206 CCTGGCGTTACCCAACTTAATCGCCTTTCAGCACATCCCGCTTTCGCCAGCTGCGTAAT 3265
DB CCTGGCGTTACCCAACTTAATCGCCTTTCAGCACATCCCGCTTTCGCCAGCTGCGTAAT 5800
QY 3266 AGCGAAGAGCGCCGACGATCGCCCTTCCAAACAGTTGCGCAGCCCTGAATGGCGAATGG 3325
DB AGCGAAGAGCGCCGACGATCGCCCTTCCAAACAGTTGCGCAGCCCTGAATGGCGAATGG 5740
QY 3326 ACGCGCCCTGTAGCGGCGATTAGCGCGCGGTGTGGTTACGCGGAGCGTGACCG 3395
DB ACGCGCCCTGTAGCGGCGATTAGCGCGCGGTGTGGTTACGCGGAGCGTGACCG 5680
QY 3386 CTACACTTGCAGCGCCCTAGCGCCGCTCCTTTTCGCTTTCTTCCCTTCTTCCCTTCGCGCA 3445
DB CTACACTTGCAGCGCCCTAGCGCCGCTCCTTTTCGCTTTCTTCCCTTCTTCCCTTCGCGCA 5620
QY 3446 CGTTTCGCGGCTTTCGCGGCTCAAGCTCTAATCGGGGCTCCCTTTAGGGTTCCGATTTA 3505
DB CGTTTCGCGGCTTTCGCGGCTCAAGCTCTAATCGGGGCTCCCTTTAGGGTTCCGATTTA 5560
QY 3506 GAGCTTTAGGCGACCTGACCGCAAAACCTTGATTTGGGTGATGTTTCAGTAGTGGC 3565
DB GAGCTTTAGGCGACCTGACCGCAAAACCTTGATTTGGGTGATGTTTCAGTAGTGGC 5500
QY 3566 CATCGCCCTGATAGACGGTTTTTCGCGCTTTGACGTTTGGAGTCCACGTTCTTTAATAGTG 3625
DB CATCGCCCTGATAGACGGTTTTTCGCGCTTTGACGTTTGGAGTCCACGTTCTTTAATAGTG 5440
QY 3626 GACTCTGTTCCAACTCGGAACAACACTCAACCCCTATCTCGGCTCTATCTTTGATTAT 3685
DB GACTCTGTTCCAACTCGGAACAACACTCAACCCCTATCTCGGCTCTATCTTTGATTAT 5380
QY 3686 AAGGATTTTCGGAATTTTCGCGCTATTGTTTAAATAATGAGCTGATTTTAAATAATTTA 3745
DB AAGGATTTTCGGAATTTTCGCGCTATTGTTTAAATAATGAGCTGATTTTAAATAATTTA 5320
QY 3746 ACGGGAATTTTAAACAAATATTAAAGTTTACAAATTCGCGCTGATCGGTAATTTCTCCTT 3805
DB ACGGGAATTTTAAACAAATATTAAAGTTTACAAATTCGCGCTGATCGGTAATTTCTCCTT 5260
QY 3806 ACCCATCTGCGGTATTTTCCACACCGCATACAGTGGCAGCTTTTCGGGGAAATGTCGCG 3865
DB ACCCATCTGCGGTATTTTCCACACCGCATACAGTGGCAGCTTTTCGGGGAAATGTCGCG 5200
QY 3866 GAACCCCTATTTGTTTATTTTCTTAATAATCAATTCAAATATGTATCCGCTCATGAGACAAT 3925
DB GAACCCCTATTTGTTTATTTTCTTAATAATCAATTCAAATATGTATCCGCTCATGAGACAAT 5140
QY 3926 AACCTGATTAATGCTTCAATAATATGAAAAAGGAGATGATGATTTCAACATTTCC 3985
DB AACCTGATTAATGCTTCAATAATATGAAAAAGGAGATGATGATTTCAACATTTCC 5080
QY 3986 GTGCGCCCTTATTTCCCTTTTTCGGGCAATTTTGCCTTCTGTTTTTGTCTACCCAGAAA 4045
DB GTGCGCCCTTATTTCCCTTTTTCGGGCAATTTTGCCTTCTGTTTTTGTCTACCCAGAAA 5020
QY 4046 CGCTGTTGAAGTAAAGATGCTGAAGATCAGTTGGTGCACGAGTGGGTACATCGAAC 4105
DB CGCTGTTGAAGTAAAGATGCTGAAGATCAGTTGGTGCACGAGTGGGTACATCGAAC 4960
QY 4106 TGGATCTCAACAGCGGTGAAGATCCTTGAGAGTTTTCGCCCGGAGAACGTTTCCAATGA 4165
DB TGGATCTCAACAGCGGTGAAGATCCTTGAGAGTTTTCGCCCGGAGAACGTTTCCAATGA 4900
QY 4166 TGAGCACTTTTAAAGTTCTGCTATGTGGCGCGTATTATCCCGTATTGACGCCGGGCAAG 4225
DB TGAGCACTTTTAAAGTTCTGCTATGTGGCGCGTATTATCCCGTATTGACGCCGGGCAAG 4840
QY 4226 AGCAACTCGCTCGCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACAGTCA 4285
DB AGCAACTCGCTCGCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACAGTCA 4780
QY 4286 CAGAAAAGCATCTTACGGATGGCATGACAGTAAAGAAATTTATGSCAGTCTGTCCTAATCA 4345
DB CAGAAAAGCATCTTACGGATGGCATGACAGTAAAGAAATTTATGSCAGTCTGTCCTAATCA 4720
QY 4346 TGAGTGATAACACTCGCGGCAACTTACTCTGACCAAGATCGGAGGACCGAAGAGCTAA 4405
DB TGAGTGATAACACTCGCGGCAACTTACTCTGACCAAGATCGGAGGACCGAAGAGCTAA 4660
QY 4406 CCGCTTTTTCGCAAAATGCGGGGATCATGTAATCTCGCTTGTGTTGGGAAACCGGAGC 4465
DB CCGCTTTTTCGCAAAATGCGGGGATCATGTAATCTCGCTTGTGTTGGGAAACCGGAGC 4600
QY 4466 TGAATGAAGCATATCAAAACGACGAGCGTGACACGATGTCCTGTAGCAATGCAACAA 4525
DB TGAATGAAGCATATCAAAACGACGAGCGTGACACGATGTCCTGTAGCAATGCAACAA 4540
QY 4526 CGTTGCGCAAACTAATTAACCTGGGAACTTACTCTAGCTTCCCGGCAACAAATTAATAG 4585
DB CGTTGCGCAAACTAATTAACCTGGGAACTTACTCTAGCTTCCCGGCAACAAATTAATAG 4480
QY 4586 ACTGGATGGAGCGGATAAAGTTTCAGGACCACTTCTGCGCTCGGCGCTTCCGCTGGCT 4645
DB ACTGGATGGAGCGGATAAAGTTTCAGGACCACTTCTGCGCTCGGCGCTTCCGCTGGCT 4420
QY 4646 GGTATTATGCTGATAAATCTGGAGCCCGTGAGCGTGTCTGCGGCTATCATTTGAGCAC 4705
DB GGTATTATGCTGATAAATCTGGAGCCCGTGAGCGTGTCTGCGGCTATCATTTGAGCAC 4360
QY 4706 TGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTTCTACACGACGGGAGTCAGGCAA 4765
DB TGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTTCTACACGACGGGAGTCAGGCAA 4300
QY 4766 CTATGGATGAACGAAATAGACAGATCGCTGAGATAGGTGCTCTACTGATTAAAGCATTTGGT 4825
DB CTATGGATGAACGAAATAGACAGATCGCTGAGATAGGTGCTCTACTGATTAAAGCATTTGGT 4240
QY 4826 AACTGTGAGCAAGATTTTACTCATATATATCTTTAGATTTGATTTAAACCTTCATTTTAAAT 4885
DB AACTGTGAGCAAGATTTTACTCATATATATCTTTAGATTTGATTTAAACCTTCATTTTAAAT 4180
QY 4886 TTAAAGGATCTAGGTGAAGATCCTTTTGTATATCTCATGACCAAAATCCCTTTAAACGTG 4945

Db 2748 GGCGGCTGGTGGTTACGCGCAGCGTGACCGCTACACTTGCAGCGCCCTAGCGCCGCG 2689
QY 3414 TCCCTTTCGCTTCTTCCCTTCTCCCTTCTCGCCACAGTTCGCGGCTTTCGCCGTCACAGCTCT 3473
Db 2688 TCCCTTTCGCTTCTTCCCTTCTCCCTTCTCGCCACAGTTCGCGGCTTTCGCCGTCACAGCTCT 2629
QY 3474 AAATCGGGGGTCCCTTTAGGTTCCGATTTAGAGCTTTACGGCACCTTCGACCGCAAAA 3533
Db 2628 AAATCGGGGGTCCCTTTAGGTTCCGATTTAGAGCTTTACGGCACCTTCGACCGCAAAA 2569
QY 3534 ACTTGATTTGGGTGATGTTTCACTGAGTGGCCATCGCCCTGATAGAGGTTTTTCGGCC 3593
Db 2568 ACTTGATTTGGGTGATGTTTCACTGAGTGGCCATCGCCCTGATAGAGGTTTTTCGGCC 2509
QY 3594 TTTGACGTTGGAGTCCACGTTCTTTAAATAGTGGACTCTTGTTCCAAAATCGGAACAACACT 3653
Db 2508 TTTGACGTTGGAGTCCACGTTCTTTAAATAGTGGACTCTTGTTCCAAAATCGGAACAACACT 2449
QY 3654 CAACCTATCTCGGTCTATTTCTTTGATTTATAGGGATTTTACGGGATTTTCCGATTTTCGGCCATTTG 3713
Db 2448 CAACCTATCTCGGTCTATTTCTTTGATTTATAGGGATTTTACGGGATTTTCCGATTTTCGGCCATTTG 2389
QY 3714 GTTAAAAAATGAGCTGATTTTAAACAAATTTTAAACGCGAATTTTAAACAAAATTTTAAACGCT 3773
Db 2388 GTTAAAAAATGAGCTGATTTTAAACAAATTTTAAACGCGAATTTTAAACAAAATTTTAAACGCT 2329
QY 3774 TACAAATTTCCGCTGATGGGTATTTTCTTCTTACGATCTGTGCGGTATTTTCAACCGCA 3833
Db 2328 TACAAATTT - CCTGATGCGGTATTTTCTTCTTACGATCTGTGCGGTATTTTCAACCGCA 2271
QY 3834 TACAGTGGCACTTTTCCGGGAAATGTGCGGGAACTTTCGCGGAACTTTCGATTTTCTTAAAT 3893
Db 2270 T - CAGTGGCACTTTTCCGGGAAATGTGCGGGAACTTTCGCGGAACTTTCGATTTTCTTAAAT 2212
QY 3894 ACATTCOAATATGATTCGCTCATGAGACAATAACCTCTGATAAATGCTTCAATATATG 3953
Db 2211 ACATTCOAATATGATTCGCTCATGAGACAATAACCTCTGATAAATGCTTCAATATATG 2152
QY 3954 AAAAGGAGATGATGATTTCAACATTTCCGTTGCGCCCTTATTCCTTTTTCGGC 4013
Db 2151 AAAAGGAGATGATGATTTCAACATTTCCGTTGCGCCCTTATTCCTTTTTCGGC 2092
QY 4014 ATTTTGCTTCTGTTTGTCTACCCAGAAACGCTGTGAAAGTAAAGATGCTGAGA 4073
Db 2091 ATTTTGCTTCTGTTTGTCTACCCAGAAACGCTGTGAAAGTAAAGATGCTGAGA 2032
QY 4074 TCAGTGGGTGCACGAGTGGTTACATCGAACTGGATCTCAACAGCGGTAAAGCTCTTGA 4133
Db 2031 TCAGTGGGTGCACGAGTGGTTACATCGAACTGGATCTCAACAGCGGTAAAGCTCTTGA 1972
QY 4134 GAGTTTTCGCCCGGAGAACGTTTTCOAATGATGAGCACTTTTAAAGTTCGTATGFG 4193
Db 1971 GAGTTTTCGCCCGGAGAACGTTTTCOAATGATGAGCACTTTTAAAGTTCGTATGFG 1912
QY 4194 CGCGTATTTATCCGTTATGACGGCGGCAAGACAACTCGGTGCGCCATACACTATTC 4253
Db 1911 CGCGTATTTATCCGTTATGACGGCGGCAAGACAACTCGGTGCGCCATACACTATTC 1852
QY 4254 TCAGAATGACTTGGTTGAGTACTCACCAGTCAACGAAAGCATCTTACGGATGGCATGAC 4313
Db 1851 TCAGAATGACTTGGTTGAGTACTCACCAGTCAACGAAAGCATCTTACGGATGGCATGAC 1792
QY 4314 AGTAAGAGAAATGTCAGTGTGCCATAACCATGATGATAAACAATCGGCGCAACTTACT 4373
Db 1791 AGTAAGAGAAATGTCAGTGTGCCATAACCATGATGATAAACAATCGGCGCAACTTACT 1732
QY 4374 TCTGACACAGATCGGAGACCGAAGGAGCTAACCGCTTTTTCGACAACTGGGGGATCA 4433
Db 1731 TCTGACACAGATCGGAGACCGAAGGAGCTAACCGCTTTTTCGACAACTGGGGGATCA 1672
QY 4434 TGTAACCTGCTTGTATGCTTGGGAAACCGGAGTGAATGAAGCCATACCAACAGCAGCG 4493

Db 1671 TGTAACCTGCTTGTATGCTTGGRAACCGGAGCTGAATGAAGCCATACCAACGACGAGCG 1612
QY 4494 TGACACACAGATGCTGTAGCAATGGCAACAAACGTTGGCGCAAACTATTAACTGGCGAACT 4553
Db 1611 TGACACACAGATGCTGTAGCAATGGCAACAAACGTTGGCGCAAACTATTAACTGGCGAACT 1552
QY 4554 ACTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGGAATGAGGCGGATAAAGTTGCGAG 4613
Db 1551 ACTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGGAATGAGGCGGATAAAGTTGCGAG 1492
QY 4614 ACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTATTTGCTGATAAATCTGGAGCGCG 4673
Db 1491 ACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTATTTGCTGATAAATCTGGAGCGCG 1432
QY 4674 TGAGCGTGGGTCTCGCGGTATCATTTGACGACTGCGGGCCAGATGTAAGCCCTCCCGTAT 4733
Db 1431 TGAGCGTGGGTCTCGCGGTATCATTTGACGACTGCGGGCCAGATGTAAGCCCTCCCGTAT 1372
QY 4734 CGTAGTTATCTACACGCGGGGAGTCAAGCACTTGGTAACTGTAGCAACAAATAGACAGATCGC 4793
Db 1371 CGTAGTTATCTACACGCGGGGAGTCAAGCACTTGGTAACTGTAGCAACAAATAGACAGATCGC 1312
QY 4794 TGAGTAGGTGCTTCACTGATTAAGCACTTGGTAACTGTAGCAACAAATAGACAGATCGC 4853
Db 1311 TGAGTAGGTGCTTCACTGATTAAGCACTTGGTAACTGTAGCAACAAATAGACAGATCGC 1252
QY 4854 ACTTTAGATGATTTAAACCTTCAATTTTAAATTTTAAAGGATCTAGGTGAAGATCCTTTT 4913
Db 1251 ACTTTAGATGATTTAAACCTTCAATTTTAAATTTTAAAGGATCTAGGTGAAGATCCTTTT 1192
QY 4914 TGATAATCTATGACCAAAATCCCTTACGCTGAGTTTTCCTTCCACTGAGCGTCAAGCC 4973
Db 1191 TGATAATCTATGACCAAAATCCCTTACGCTGAGTTTTCCTTCCACTGAGCGTCAAGCC 1132
QY 4974 CGTAGAAAAGATCAAGGATCTTCTTGAGATCTTCTTTCGCGGTAATCTGCTGCTT 5033
Db 1131 CGTAGAAAAGATCAAGGATCTTCTTGAGATCTTCTTTCGCGGTAATCTGCTGCTT 1072
QY 5034 GCAACAAAAAACAACCGCTTACAGCGGTGGTTTGGTTGCGGATCAAGAGTCAACAC 5093
Db 1071 GCAACAAAAAACAACCGCTTACAGCGGTGGTTTGGTTGCGGATCAAGAGTCAACAC 1012
QY 5094 TCTTTTTCGAGGTAAGTGGCTTACAGAGCGGAGTCAACAACTGCTTCTTCTAGT 5153
Db 1011 TCTTTTTCGAGGTAAGTGGCTTACAGAGCGGAGTCAACAACTGCTTCTTCTAGT 952
QY 5154 GTAGCGGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCT 5213
Db 951 GTAGCGGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCT 892
QY 5214 GCTAATCTGTTACAGTGGCTGCTGCGAGTGGCGATAAGTGGTCTTACCGGTTGGA 5273
Db 891 GCTAATCTGTTACAGTGGCTGCTGCGAGTGGCGATAAGTGGTCTTACCGGTTGGA 832
QY 5274 CTCAGACGATAGTTACCGGATAGGCGGAGTGGCTGCGGCTGAAACGGGGGTTGCGCAC 5333
Db 831 CTCAGACGATAGTTACCGGATAGGCGGAGTGGCTGCGGCTGAAACGGGGGTTGCGCAC 772
QY 5334 ACAGCCAGCTTTGAGCGAAACGACTTACACGAACTGAGATACCTACAGCTGAGCTATG 5393
Db 771 ACAGCCAGCTTTGAGCGAAACGACTTACACGAACTGAGATACCTACAGCTGAGCTATG 712
QY 5394 AGAAGCGCAACGTTTCCGAAAGGAGAAAGGCGGACAGGTTATCCGTTAAGCGGACGGT 5453
Db 711 AGAAGCGCAACGTTTCCGAAAGGAGAAAGGCGGACAGGTTATCCGTTAAGCGGACGGT 652
QY 5454 CGGAAACGAGGAGCGCAGGAGGAGCTTCCAGGGGAAAACGCTGATCTTTTATAGTCC 5513
Db 651 CGGAAACGAGGAGCGCAGGAGGAGCTTCCAGGGGAAAACGCTGATCTTTTATAGTCC 592
QY 5514 TGTCCGGTTTTCGCCACCTCTGACTTGGAGCTGCAATTTTGTGATGCTGTCAGGGGGCG 5573
Db 591 TGTCCGGTTTTCGCCACCTCTGACTTGGAGCTGCAATTTTGTGATGCTGTCAGGGGGCG 532


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QY 4014 ATTTTGGCTTCCCTGTTTGGCTTACCCAGAAACGCTGGTGAAGTAAAGTGTCTGAAGA 4073
Db 2091 ATTTTGGCTTCCCTGTTTGGCTTACCCAGAAACGCTGGTGAAGTAAAGTGTCTGAAGA 2032
QY 4074 TCAGTTGGGTGTCAGAGTGGGTATCATCTGAACCTGATCTCAACAGCGGTAAAGTCTCTTGA 4133
Db 2031 TCAGTTGGGTGTCAGAGTGGGTATCATCTGAACCTGATCTCAACAGCGGTAAAGTCTCTTGA 1972
QY 4134 GAGTTTGGCCCGAAGAAAGTTTCCAAATGATGAGCACTTTTAAAGTCTTGTATGTGG 4193
Db 1971 GAGTTTGGCCCGAAGAAAGTTTCCAAATGATGAGCACTTTTAAAGTCTTGTATGTGG 1912
QY 4194 GCGGTATATCCCGTATTTGACCGCGGCGRAGACCACTCGTCCGCGCATACACTATTC 4253
Db 1911 GCGGTATATTTCCCGTATTTGACCGCGGCGRAGACCACTCGTCCGCGCATACACTATTC 1852
QY 4254 TCAGATGACTTGGTTGAGTACTCACAGTCAACAGAAAGCATCTTACGGATGGCATGAC 4313
Db 1851 TCAGATGACTTGGTTGAGTACTCACAGTCAACAGAAAGCATCTTACGGATGGCATGAC 1792
QY 4314 AGTAAGAAATATGAGTGCTGCATAAACCATGAGTGATTAACACTGGCGGCAACTTACT 4373
Db 1791 AGTAAGAAATATGAGTGCTGCATAAACCATGAGTGATTAACACTGGCGGCAACTTACT 1732
QY 4374 TCTGACAAACGATCGGAGCGGAGGAGCTAACCGCTTTTTCACAACTGGGGGATCA 4433
Db 1731 TCTGACAAACGATCGGAGCGGAGGAGCTAACCGCTTTTTCACAACTGGGGGATCA 1672
QY 4434 TGTAACTCGCCTTGATCGTTGGGAAACGAGCTGAATGAAGCCCATACCAACAGCGAGCG 4493
Db 1671 TGTAACTCGCCTTGATCGTTGGGAAACGAGCTGAATGAAGCCCATACCAACAGCGAGCG 1612
QY 4494 TGACACACGATGCTGAGCAATGGGCAACAACTGGCGCAAACTATTAACCTGGCGAACT 4553
Db 1611 TGACACACGATGCTGAGCAATGGGCAACAACTGGCGCAAACTATTAACCTGGCGAACT 1552
QY 4554 ACTTACTCTAGCTTCCGGCAACAAATTAATAGACTGGATGAGCGGATTAAGTTGCGAGG 4613
Db 1551 ACTTACTCTAGCTTCCGGCAACAAATTAATAGACTGGATGAGCGGATTAAGTTGCGAGG 1492
QY 4614 ACCACTTCTGGCTCGGCCCTTCGCGCTGGCTGTTTATGCTGATAACTCTGGAGCGGG 4673
Db 1491 ACCACTTCTGGCTCGGCCCTTCGCGCTGGCTGTTTATGCTGATAACTCTGGAGCGGG 1432
QY 4674 TGAGCGTGGGTCTCGCGTATCATGTCAGCACTGGGCGAGATGATGAAGCCCTCCCGTAT 4733
Db 1431 TGAGCGTGGGTCTCGCGTATCATGTCAGCACTGGGCGAGATGATGAAGCCCTCCCGTAT 1372
QY 4734 CGTAGTTATCTACACGCGGGGAGTCAAGCACTATGGATGAACGAATAGACAGATCGC 4793
Db 1371 CGTAGTTATCTACACGCGGGGAGTCAAGCACTATGGATGAACGAATAGACAGATCGC 1312
QY 4794 TGAGATAGGTGCTCACTGATTAAGCACTTGGTAAGTGTGAGCACTGTCAGACCAAGTTTACTCATATAT 4853
Db 1311 TGAGATAGGTGCTCACTGATTAAGCACTTGGTAAGTGTGTCAGACCAAGTTTACTCATATAT 1252
QY 4854 ACTTTAGATTGATTTAAACCTTCAATTTTAAATTTTAAAGGATCTAGGTGAAGATCCTTTT 4913
Db 1251 ACTTTAGATTGATTTAAACCTTCAATTTTAAATTTTAAAGGATCTAGGTGAAGATCCTTTT 1192
QY 4914 TGATATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCC 4973
Db 1191 TGATATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCC 1132
QY 4974 CGTAGAAAGATCAAGGATCTTCTTGAGATCCTTTTCTGCGCGTAACTCTGCTGCTT 5033
Db 1131 CGTAGAAAGATCAAGGATCTTCTTGAGATCCTTTTCTGCGCGTAACTCTGCTGCTT 1072
QY 5034 GCAACCAAAAAACCAACCGCTTACACGCGTGGTTTGGTTTGGCGGATCAAGAGCTACCAAC 5093
Db 1071 GCAACCAAAAAACCAACCGCTTACACGCGTGGTTTGGTTTGGCGGATCAAGAGCTACCAAC 1012
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QY 5094 TCTTTTCCGAAGTAACTGCTTTCAGCAGAGCGCAGATACCAAACTACTGCTCTCTAGT 5153
Db 1011 TCTTTTCCGAAGTAACTGCTTTCAGCAGAGCGCAGATACCAAACTACTGCTCTCTAGT 952
QY 5154 GTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCT 5213
Db 951 GTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCT 892
QY 5214 GCTAATCTGTATTACAGTGGCTGCTGCCAGTAGGGGATAAGTCTGTCTTACCGGTTTGA 5273
Db 891 GCTAATCTGTATTACAGTGGCTGCTGCCAGTAGGGGATAAGTCTGTCTTACCGGTTTGA 832
QY 5274 CTCGAAGCAGATAGTTACCGGATAAGCGCAGCGTTCGGGCTGAACGGGGGTTTGTGCAC 5333
Db 831 CTCGAAGCAGATAGTTACCGGATAAGCGCAGCGTTCGGGCTGAACGGGGGTTTGTGCAC 772
QY 5334 ACAGCCAGCTTGGAGCGAAACGACTACACCGAACTGAGATACCTACAGCGTGAAGTATG 5393
Db 771 ACAGCCAGCTTGGAGCGAAACGACTACACCGAACTGAGATACCTACAGCGTGAAGTATG 712
QY 5394 AGAAGCGCCACGCTTCCGNAAGGAGAAAGCGGACAGGTATCGGTAAAGCGCAGGCT 5453
Db 711 AGAAGCGCCACGCTTCCGNAAGGAGAAAGCGGACAGGTATCGGTAAAGCGCAGGCT 652
QY 5454 CGGAACAGGAGAGCGCAGCGGAGCTTCCAGGGGGAACCGCTGGTATCTTTATAGTCC 5513
Db 651 CGGAACAGGAGAGCGCAGCGGAGCTTCCAGGGGGAACCGCTGGTATCTTTATAGTCC 592
QY 5514 TGTGGGTTTTCGCCACCTCTGACTTTGAGCGTTCGATTTTGTGATGCTCGTCAGGGGGCG 5573
Db 591 TGTGGGTTTTCGCCACCTCTGACTTTGAGCGTTCGATTTTGTGATGCTCGTCAGGGGGCG 532
QY 5574 GAGCTATGAAAGAAACCGCAGACAGCGGCTTTTACGGTCTCTGGCTTTTGTGCGCC 5633
Db 531 GAGCTATGAAAGAAACCGCAGACAGCGGCTTTTACGGTCTCTGGCTTTTGTGCGCC 472
QY 5634 TTTTGTCTCACATGTTCTTTCTGCTGTTATCCCTGATTCTCTGATTAACCGTATTACCGC 5693
Db 471 TTTTGTCTCACATGTTCTTTCTGCTGTTATCCCTGATTCTCTGATTAACCGTATTACCGC 412
QY 5694 CTTTGAAGTGAAGTATGATACCGCTCCGCGCAGCGCAACCGCAGCGCAGCGAGTCAAGT 5753
Db 411 CTTTGAAGTGAAGTATGATACCGCTCCGCGCAGCGCAACCGCAGCGCAGCGAGTCAAGT 352
QY 5754 CGAGAAAGCGAAGAGCGCCCAATACGCAACCGGCTCTCCCGCGGTTGGCCGATTCA 5813
Db 351 CGAGAAAGCGAAGAGCGCCCAATACGCAACCGGCTCTCCCGCGGTTGGCCGATTCA 292
QY 5814 TTAATGCAG 5822
Db 291 TTAATGCAG 283

RESULT 11
ADA94775/c
ID ADA94775 standard; DNA; 4514 BP.
XX
AC ADA94775;
XX
DT 20-NOV-2003 (first entry)
XX
DE Plasmid pGL2neo (+) #SEQ ID 4.
XX
KW Lymphocyte; vertebrate; antibody; genetically modified; ds.
XX
OS Synthetic.
XX
PN EPI321477-A1.
XX
PD 25-JUN-2003.
XX
PF 22-DEC-2001; 2001EP-00130805.
XX
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PR 22-DEC-2001; 2001EP-00130805.

XX (GRAW/) GRAWUNDER U.

PA (MELC/) MELCHERS G F.

XX Grawunder U, Melchers GF;

XX WPI; 2003-571360/54.

DR

XX Generating genetically modified vertebrate precursor lymphocytes for
PT producing any heterologous antibody or binding protein comprises
PT effecting differentiation of the precursor lymphocytes into mature
PT lymphoid lineage cells.

XX Example 5; Page 49-51; 111pp; English.

XX The invention relates to a method for generating vertebrate lymphocytes
CC that can be used for the production of any heterologous antibody, antigen
CC receptor, artificial binding protein, or their functional fragments. The
CC method of the invention comprises genetically modifying vertebrate
CC precursor lymphocytes, and effecting differentiation of the precursor
CC lymphocytes into mature lymphoid lineage cells either in vitro or in
CC vivo. The method and the genetically modified and differentiated
CC vertebrate lymphocytes are useful in the production of any heterologous
CC antibody, artificial binding protein, antigen receptor, or their
CC fragments, where the antibody is monoclonal or polyclonal, or partially
CC resembles a human antibody, binding protein or antigen receptor. The
CC antibodies are useful for the diagnosis, prevention and treatment of
CC diseases. The method combines the advantages of both the phage display
CC system (i.e. speed and flexibility in generating human antibodies, and
CC the ability to modify and improve the properties of existing antibodies),
CC and of the human immunoglobulin transgenic mouse technology (i.e. the
CC ability to obtain high affinity antibodies due to affinity maturation
CC occurring in the immune system, and the production antibodies with
CC physiologic and natural structural features). The current sequence
CC represents the plasmid sequence pGh2neo (+). This sequence is used in an
CC example from the invention as a template for the amplification of loxp
CC site flanked neomycin.

XX Sequence 4514 BP; 1108 A; 1184 C; 1171 G; 1051 T; 0 U; 0 Other;

Query Match 45.8%; Score 2668.6; DB 8; Length 4514;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 2677; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 3132 GGCCCAATTCGCCCTATAGTACGTCGTATTACAAATTCACCTGGCGCTGTTTACAACGTC 3191

DB 4514 GGCCCAATTCGCCCTATAGTACGTCGTATTACAAATTCACCTGGCGCTGTTTACAACGTC 4455

QY 3192 GTGACTGGGAAACCCCTGGCGTTACCCAACTTAATCGCCTTGACGACATFCCCCCTTTCG 3251

DB 4454 GTGACTGGGAAACCCCTGGCGTTACCCAACTTAATCGCCTTGACGACATFCCCCCTTTCG 4395

QY 3252 CCAGCTGGCGTATAGCGAGAGCGCCGACCGATCGCCCTTCCACAGCTTGGCGAGCC 3311

DB 4394 CCAGCTGGCGTATAGCGAGAGCGCCGACCGATCGCCCTTCCACAGCTTGGCGAGCC 4335

QY 3312 TGAATGCGGAATGGAGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGGTGTAC 3371

DB 4334 TGAATGCGGAATGGAGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGGTGTAC 4275

QY 3372 GCGCAGCGTACCGCTACCTTCCAGCGCCCTAGCGCGCTTCCCTTTCGCTTTCCTCC 3431

DB 4274 GCGCAGCGTACCGCTACCTTCCAGCGCCCTAGCGCGCTTCCCTTTCGCTTTCCTCC 4215

QY 3432 TTCCTTTCCTCGCACGTTCCCGGCTTTCCTCGCTCAAGCTCTAAATCGGGGCTCCCTTT 3491

DB 4214 TTCCTTTCCTCGCACGTTCCCGGCTTTCCTCGCTCAAGCTCTAAATCGGGGCTCCCTTT 4155

QY 3492 AGGGTTCCGATTTAGAGCTTTACGGCACCTCGACCGCAAAAACCTTGATTTGGGTGATGG 3551

DB 4154 AGGGTTCCGATTTAGAGCTTTACGGCACCTCGACCGCAAAAACCTTGATTTGGGTGATGG 4095

QY 3552 TTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTTCGCCCTTTGACGTTGGAGTCCAC 3611
DB 4094 TTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTTCGCCCTTTGACGTTGGAGTCCAC 4035
QY 3612 GTTCTTTAATAGTGGACTCTTGTTCMAAAGTGAACAACTCAACCTATCTCGGTCTA 3671
DB 4034 GTTCTTTAATAGTGGACTCTTGTTCMAAAGTGAACAACTCAACCTATCTCGGTCTA 3975
QY 3672 TTCCTTTGATTTAATAGGGATTTTTCGGCTATTTGGTTTAAAAAATGAGCTGAT 3731
DB 3974 TTCCTTTGATTTAATAGGGATTTTTCGGCTATTTGGTTTAAAAAATGAGCTGAT 3915
QY 3732 TTAACAAATATTTAAGCGGAATTTTAAACAAATATTTAAGCTTTTACAAATTTTCGCTGATGC 3791
DB 3914 TTAACAAATATTTAAGCGGAATTTTAAACAAATATTTAAGCTTTTACAAATTTTCGCTGATGC 3855
QY 3792 GGTATTTTCTCCTTAGCATCTGTGGGTATTTTACACCGCATACAGGTGGCATTTTCG 3851
DB 3854 GGTATTTTCTCCTTAGCATCTGTGGGTATTTTACACCGCATACAGGTGGCATTTTCG 3795
QY 3852 GGGAAATGTGCGCGGAACCCCTAATTTTATTTTCTAAATACATTTCAAAATATGATGCC 3911
DB 3794 GGGAAATGTGCGCGGAACCCCTAATTTTATTTTCTAAATACATTTCAAAATATGATGCC 3735
QY 3912 GCTCATGAGACAATAACCCCTGATAAATGCTTCAATAATATTTGAAAAAGGAGATGATGAG 3971
DB 3734 GCTCATGAGACAATAACCCCTGATAAATGCTTCAATAATATTTGAAAAAGGAGATGATGAG 3675
QY 3972 TATTCACATTTCCGTTGTGCCCTTATTCCTTTTTCGGCAATTTTTCCTTCTGTTTT 4031
DB 3674 TATTCACATTTCCGTTGTGCCCTTATTCCTTTTTCGGCAATTTTTCCTTCTGTTTT 3615
QY 4032 TGCTCACCCAGAAACCCCTGTGAAAGTAAAGATGCTGAAGATCAGTTGGTGCACGAGT 4091
DB 3614 TGCTCACCCAGAAACCCCTGTGAAAGTAAAGATGCTGAAGATCAGTTGGTGCACGAGT 3555
QY 4092 GGGTTACATCGAATCGATCTCAACAGCGGTAAAGATCTTTGAGAGTTTTTCGCCCCGAAGA 4151
DB 3554 GGGTTACATCGAATCGATCTCAACAGCGGTAAAGATCTTTGAGAGTTTTTCGCCCCGAAGA 3495
QY 4152 AGCTTTTCCAAATGATGAGCACCTTTTAAAGTTCTGCTATGTGGCGCGGTATTTATCCCGTAT 4211
DB 3494 AGCTTTTCCAAATGATGAGCACCTTTTAAAGTTCTGCTATGTGTATCATATATATCCCGTAT 3435
QY 4212 TGACGCGCGGCAAGAGCAACTCGGTCCGCGCATACACTATTCTCAGAATGACTTGGTTGA 4271
DB 3434 TGACGCGCGGCAAGAGCAACTCGGTCCGCGCGCGGTATTTCTCAGAAATGACTTGGTTGA 3375
QY 4272 GTACTCACAGTCAAGAAAAGCATCTTACCGATGGCATGACAGTAAGAGAAATATGCGAG 4331
DB 3374 GTACTCACAGTCAAGAAAAGCATCTTACCGATGGCATGACAGTAAGAGAAATATGCGAG 3315
QY 4332 TGCTGCCATAACCATGAGTGATAACACTCGGCCCACTTACTTCTGACACAGATCGGAGG 4391
DB 3314 TGCTGCCATAACCATGAGTGATAACACTCGGCCCACTTACTTCTGACACAGATCGGAGG 3255
QY 4392 ACCGAAGAGTAAACCGCTTTTTCACAACTAGGGGGATCATGTAACTCGCCTTGATCG 4451
DB 3254 ACCGAAGAGTAAACCGCTTTTTCACAACTAGGGGGATCATGTAACTCGCCTTGATCG 3195
QY 4452 TTGGGAACCGAGCTGAATGAAGCCATACAAACGACGAGCGGTGACACAGATGCTGT 4511
DB 3194 TTGGGAACCGAGCTGAATGAAGCCATACAAACGACGAGCGGTGACACAGATGCTGT 3135
QY 4512 AGCAATGGCAACAACTGTGCGAAACTATTAACTGCGCACTACTTACTTACTTCTCCG 4571
DB 3134 AGCAATGGCAACAACTGTGCGAAACTATTAACTGCGCACTACTTACTTACTTCTCCG 3075
QY 4572 GCAACAATTAATAGACTGATGAGCGGATAAAGTTGACGACCACTTCTCGCTCGGC 4631
DB 3074 GCAACAATTAATAGACTGATGAGCGGATAAAGTTGACGACCACTTCTCGCTCGGC 3015
QY 4632 CCTTCCGGTGGCTGTTTATTTGCTGATAAATCTGAGCGCGGTGAGGTGCTCGCGG 4691

Db 3014 CTTCCGCGCTGGCTGTTTATGCTGATTAATCTGAGCGGTGAGCGTGGTCTCGGG 2955
QY 4692 TATCATTCAGACACTGGGGCGAGATGTTAAAGCCCTCCCGTATCGTAGTTATCTACACGAC 4751
Db 2954 TATCATTCAGACACTGGGGCGAGATGTTAAAGCCCTCCCGTATCGTAGTTATCTACACGAC 2895
QY 4752 GGGAGTCCAGGCAACTATGAGTGAACGAAATAGACAGATCGTAGATAGGTGCTCACT 4811
Db 2894 GGGAGTCCAGGCAACTATGAGTGAACGAAATAGACAGATCGTAGATAGGTGCTCACT 2835
QY 4812 GATTAAGCATTTGTTAAAGGATCTAGTGAAGATCTCTTTTGTATATCTCATGACCA 4931
Db 2834 GATTAAGCATTTGTTAAAGGATCTAGTGAAGATCTCTTTTGTATATCTCATGACCA 2775
QY 4872 ACTTCATTTTAAATTTAAAGGATCTAGTGAAGATCTCTTTTGTATATCTCATGACCA 4931
Db 2774 ACTTCATTTTAAATTTAAAGGATCTAGTGAAGATCTCTTTTGTATATCTCATGACCA 2715
QY 4932 AATCCCTTAAAGCTGAGTTTCTGTTCCACTGAGCGTCAAGCCCGTAGAAAAGATCAAGG 4991
Db 2714 AATCCCTTAAAGCTGAGTTTCTGTTCCACTGAGCGTCAAGCCCGTAGAAAAGATCAAGG 2655
QY 4992 ATCTCTTTGAGATCCTTTTCTGCGGTAACTCTGCTGTTGCAACAAAAAACCCACC 5051
Db 2654 ATCTCTTTGAGATCCTTTTCTGCGGTAACTCTGCTGTTGCAACAAAAAACCCACC 2595
QY 5052 GCTACACGGTGGTGTGTTGTCGGGATCAAGAGCTACCACTCTTTTCCGAAAGTAAAC 5111
Db 2594 GCTACACGGTGGTGTGTTGTCGGGATCAAGAGCTACCACTCTTTTCCGAAAGTAAAC 2535
QY 5112 TGGCTTACGAGAGCGGAGATACAAATACCTGCTCTCTAGTGTAGCGGTAGGCGCA 5171
Db 2534 TGGCTTACGAGAGCGGAGATACAAATACCTGCTCTCTAGTGTAGCGGTAGGCGCA 2475
QY 5172 CCACCTTCAAGAACTCTGTAGCACCGCTACATCCTGCTCTGCTAATCTCTGTACCACT 5231
Db 2474 CCACCTTCAAGAACTCTGTAGCACCGCTACATCCTGCTCTGCTAATCTCTGTACCACT 2415
QY 5232 GGCTGCTCCAGTGGCGATAGTGTCTTACCGGTTGAGCTCAAGACGATAGTTACC 5291
Db 2414 GGCTGCTCCAGTGGCGATAGTGTCTTACCGGTTGAGCTCAAGACGATAGTTACC 2355
QY 5292 GGATAAGCGGAGCGGTCGGCTGAAACGGGGGTTCTGTCACAGCCAGCTTGGAGCG 5351
Db 2354 GGATAAGCGGAGCGGTCGGCTGAAACGGGGGTTCTGTCACAGCCAGCTTGGAGCG 2295
QY 5352 AACGACCTTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCAGCTTCC 5411
Db 2294 AACGACCTTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCAGCTTCC 2235
QY 5412 CGAAGGGAGAAAGCGGAGACAGGTATCGGTAAGCGGCAAGGTTCGGAACAGGAGCGCAC 5471
Db 2234 CGAAGGGAGAAAGCGGAGACAGGTATCGGTAAGCGGCAAGGTTCGGAACAGGAGCGCAC 2175
QY 5472 GAGGAGCTTCCAGGGGAAAGCGCTGATCTTTATAGTCTCTGCGGTTTCGCCACT 5531
Db 2174 GAGGAGCTTCCAGGGGAAAGCGCTGATCTTTATAGTCTCTGCGGTTTCGCCACT 2115
QY 5532 CTGACTTGAGCGTCAATTTTGTGATGCTCTGAGGGGGGCGAGCCCTATGGAAGAAAGCG 5591
Db 2114 CTGACTTGAGCGTCAATTTTGTGATGCTCTGAGGGGGGCGAGCCCTATGGAAGAAAGCG 2055
QY 5592 CAGCAACGCGGCTTTTACGGTCTCGGCTCTTTTGTGCGGCTTTTGTGCTACATGTTCTT 5651
Db 2054 CAGCAACGCGGCTTTTACGGTCTCTGCGGCTTTTGTGCGGCTTTTGTGCTACATGTTCTT 1995
QY 5652 TCCTGCGTTATCCCTGATCTGTTGGAACCGTATTTACCGCTTTTGTGAGTCACTGATAC 5711
Db 1994 TCCTGCGTTATCCCTGATCTGTTGGAACCGTATTTACCGCTTTTGTGAGTCACTGATAC 1935
QY 5712 CGCTCGCGCGACCGCAACGACCGAGCGCAGCGAGTCACTGAGCGAGGAGCGGAGAGCG 5771

Db 1934 CGCTCGCGCGACCGAACGACGACGAGCGAGCTCAGTGCAGGAGCGAAGCGG 1875
QY 5772 CCCAATACGAAACCGCTCTCCCGCGCGCTTCCCGCGGTTGGCGGATTCATTATGACG 5822
Db 1874 CCCAATACGAAACCGCTCTCCCGCGCGCTTCCCGCGGTTGGCGGATTCATTATGACG 1824
RESULT 12
ABK11039
ID ABK11039 standard; DNA; 9359 BP.
XX AC ABK11039;
XX AC ABK11039;
DT 05-JUN-2002 (first entry)
XX pVDH636 vector containing Arabidopsis Ath1 gene.
DE pVDH636 vector; circular; cyclic; grass; plant; herbicide resistance;
KW baseball; cricket; football; golf; rugby; soccer; tennis; lawn; park;
KW athletic field; animal feedstuff; grass flowering inhibitor; Ath1; gene;
KW ds.
XX Arabidopsis thaliana.
OS Zea mays.
OS Agrobacterium tumefaciens.
OS Oryza sativa.
OS Escherichia coli.
OS Cauliflower mosaic virus.
XX Synthetic.
FH Key Location/Qualifiers
FT CDS 4930..6360
FT /*tag= a
FT /product= "Ath1"
FT /partial
FT /note= "No stop codon"
XX WO200214524-A2.
PD 21-FEB-2002.
XX 16-AUG-2001; 2001WO-EP009572.
XX 18-AUG-2000; 2000US-0226422P.
PR 27-NOV-2000; 2000US-0253274P.
PR 27-NOV-2000; 2000US-0253327P.
PR 22-JUN-2001; 2001US-0300220P.
XX (ADVA-) ADVANTA SEEDS BV.
XX Van Der Valk P, Van Dun CMP, Smeekens SCM, Proveniers MCG;
PI WPI; 2002-257611/30.
XX P-PSDB; AAU76514.
XX New genetically modified grasses that express inhibited generative
PT propagation, or herbicide resistance, useful for forage (e.g. cattle
PT feedstuff) or amenity purposes (e.g. for use in an athletic field, lawn
PT or park).
XX Example 1; Fig 6; 56pp; English.
XX The invention relates to a grass plant, which has been genetically
CC modified to substantially inhibit generative propagation and carry
CC herbicide resistance. The grass is useful for growth and/or propagation
CC of grasses. The grass is used to play at least one sport (e.g. baseball,
CC cricket, football, golf, rugby, soccer or tennis), or used at least in a
CC portion of an athletic field, lawn or park. The grass is fed to animal
CC (e.g. cattle, goat, horse or sheep) or used as an animal feedstuff. The
CC present sequence represents the coding sequence of pVDH636 vector
CC containing the Arabidopsis Ath1 gene, which was used to inhibit flowering
CC in grasses

SQ	Sequence	9359 BP; 2377 A; 2222 C; 2133 G; 2624 T; 0 U; 3 Other;
Query Match	45.7%;	Score 2658.4; DB 6; Length 9359;
Best Local Similarity	99.7%;	Pred. No. 0;
Matches 2685; Conservative	0;	Mismatches 6; Indels 3; Gaps 2;
QY	3129	TCGGGCCCCAATTCGCCCTATAGTAGAGTCGATTAACAAATCACTGCGCGTTCGTTTACAAC 3188
Db	4	TCGGGCCCCAATTCGCCCTATAGTAGAGTCGATTAACAAATCACTGCGCGTTCGTTTACAAC 63
QY	3189	GTGCTGACATGGGAAAAACCTCGGCTTACCCAACTTAATCGCCTTGACGACATCCGCCCTT 3248
Db	64	GTGCTGACATGGGAAAAACCTCGGCTTACCCAACTTAATCGCCTTGACGACATCCGCCCTT 123
QY	3249	TCGCCAGCTGCGTAAATAGCAAGAGAGCCGCGACCGATCGCCCTCCCBACAGTTGGCA 3308
Db	124	TCGCCAGCTGCGTAAATAGCAAGAGAGCCGCGACCGATCGCCCTCCCBACAGTTGGCA 183
QY	3309	GCCTGAATGGCGAATGAGCGGCCCTGTAGCGCGCAATTAAGCGCGCGGCTGTGTGGT 3368
Db	184	GCCTGAATGGCGAATGAGCGGCCCTGTAGCGCGCAATTAAGCGCGCGGCTGTGTGGT 243
QY	3369	TAGCGGAGCGTGACCGCTACATTCGCGAGCGCCTAGCGCCCTCCTTCGCTTTCCT 3428
Db	244	TAGCGGAGCGTGACCGCTACATTCGCGAGCGCCTAGCGCCCTCCTTCGCTTTCCT 303
QY	3429	CCCTTCCTTTCGCGCAGCTTCGCCGCTTCCCGTCAAGCTTAATCGGCGGCTCCC 3488
Db	304	CCCTTCCTTTCGCGCAGCTTCGCCGCTTCCCGTCAAGCTTAATCGGCGGCTCCC 363
QY	3489	TTTAGGCTTCGATTTAGAGCTTTACCGCACCTCGACCGCAAAACTTGATTTGGGTGA 3548
Db	364	TTTAGGCTTCGATTTAGAGCTTTACCGCACCTCGACCGCAAAACTTGATTTGGGTGA 423
QY	3549	TGFTACGAGTGGGCGATCGCCCTGATAGACGGTTCGCGCTTGACGTTGGAGTC 3608
Db	424	TGFTACGAGTGGGCGATCGCCCTGATAGACGGTTCGCGCTTGACGTTGGAGTC 483
QY	3609	CAGCTTCCTTAATAGTAGTGCATCTGTTCCTCAACCTGGAAACACACTCAACCCCTATCTCGT 3668
Db	484	CAGCTTCCTTAATAGTAGTGCATCTGTTCCTCAACCTGGAAACACACTCAACCCCTATCTCGT 543
QY	3669	CTATTCCTTTGATTTAAGGGAATTTGCCGATTTCCGCTTATTTGGTTAAAAAATGAGCT 3728
Db	544	CTATTCCTTTGATTTAAGGGAATTTGCCGATTTCCGCTTATTTGGTTAAAAAATGAGCT 603
QY	3729	GATTTAAACAAATTTAACGCGAATTTTAAACAAATATTAACGCTTACAATTT--CCTGA 3788
Db	604	GATTTAAACAAATTTAACGCGAATTTTAAACAAATATTAACGCTTACAATTT--CCTGA 661
QY	3789	TGCGGTATTTCTCCTTACGCATCTGCGGTATTTTCAACCGCATACAGGTGGCCTTT 3848
Db	662	TGCGGTATTTCTCCTTACGCATCTGCGGTATTTTCAACCGCATACAGGTGGCCTTT 720
QY	3849	TCGGGGAATGTCGCGGAACCCCTATTTGTTTATTTTCTTAAATATACATTCAAATATGTA 3908
Db	721	TCGGGGAATGTCGCGGAACCCCTATTTGTTTATTTTCTTAAATATACATTCAAATATGTA 780
QY	3909	TCCGCTATGAGCAATTAACCTGATTAATGCTTCAATAATTTGAAAAGGAAAGATAT 3968
Db	781	TCCGCTATGAGCAATTAACCTGATTAATGCTTCAATAATTTGAAAAGGAAAGATAT 840
QY	3969	GAGTATTCAAATTTCCGCTGCGCCCTTATTCCTTTTTCGCGCATTTTCCTTCCTGT 4028
Db	841	GAGTATTCAAATTTCCGCTGCGCCCTTATTCCTTTTTCGCGCATTTTCCTTCCTGT 900
QY	4029	TTTTGCTACCCGAAACCGTGGTGAAGTAAAGATGCTGAAAGATCAAGTTGGGTGACG 4088
Db	901	TTTTGCTACCCGAAACCGTGGTGAAGTAAAGATGCTGAAAGATCAAGTTGGGTGACG 960
QY	4089	AGTGGTTCATCGAATCGATTCACAGCGGTAAAGATCCTTGAGAGTTTTCGCCCGGA 4148
Db	961	AGTGGTTCATCGAATCGATTCACAGCGGTAAAGATCCTTGAGAGTTTTCGCCCGGA 1020
QY	4149	AGAACGTTTTCCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGGTATTAATCCCG 4208
Db	1021	AGAACGTTTTCCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGGTATTAATCCCG 1080
QY	4209	TATTGACGCGGCAAGAGCAACTCGGTGCGCCATACACTATCTCAGAAATGACTTGGT 4268
Db	1081	TATTGACGCGGCAAGAGCAACTCGGTGCGCCATACACTATCTCAGAAATGACTTGGT 1140
QY	4269	TGAGTACTCACCAGTCACAGAAAGCATCTTACGATGGCATGACAGTAAGAGAAATATG 4328
Db	1141	TGAGTACTCACCAGTCACAGAAAGCATCTTACGATGGCATGACAGTAAGAGAAATATG 1200
QY	4329	CAGTGTCTGCATTAACCATGATGATAACACTGCGGCCAACTTACTTCTGAACAAGATCGG 4388
Db	1201	CAGTGTCTGCATTAACCATGATGATAACACTGCGGCCAACTTACTTCTGAACAAGATCGG 1260
QY	4389	AGAACCGAAGAGCTTAACCGCTTTTTCGACAACTGGGGGATCATGTAATCGCCTTGA 4448
Db	1261	AGAACCGAAGAGCTTAACCGCTTTTTCGACAACTGGGGGATCATGTAATCGCCTTGA 1320
QY	4449	TCGTTGGGAACCGGAGCTGAATCAAGCATACCAACGACGAGCGTGACACACGATGCC 4508
Db	1321	TCGTTGGGAACCGGAGCTGAATCAAGCATACCAACGACGAGCGTGACACACGATGCC 1380
QY	4509	TGTAGCAATGGCAACCAACGTTTGGCGAACTATTAACTGGCGAACTACTTACTCTAGCTTC 4568
Db	1381	TGTAGCAATGGCAACCAACGTTTGGCGAACTATTAACTGGCGAACTACTTACTCTAGCTTC 1440
QY	4569	CCGGCAACAATTAATAGACTGGATGGAGCGGATTAAGTTGCAGACCACTCTTCCGCTC 4628
Db	1441	CCGGCAACAATTAATAGACTGGATGGAGCGGATTAAGTTGCAGACCACTCTTCCGCTC 1500
QY	4629	GGCCCTTCGCGTGGCTGTTTATTGCTGATAAATCTGGAGCCGCTGAGCGTGGTCTCG 4688
Db	1501	GGCCCTTCGCGTGGCTGTTTATTGCTGATAAATCTGGAGCCGCTGAGCGTGGTCTCG 1560
QY	4689	CGGTATCATTTGCAGCACTGGCGGCAGATGTAAGCCCTCCCGTATCGTAGTTATCTAC 4748
Db	1561	CGGTATCATTTGCAGCACTGGCGGCAGATGTAAGCCCTCCCGTATCGTAGTTATCTAC 1620
QY	4749	GACGGGAGTCAGGCACTATGATGAACGAATAGACAGATCGCTGAGTAGTGGCTC 4808
Db	1621	GACGGGAGTCAGGCACTATGATGAACGAATAGACAGATCGCTGAGTAGTGGCTC 1680
QY	4809	ACTGATTAAGCATTTGGTAACTGTGACAGCAAGTTTACTCATATATACCTTAGATTGATTT 4868
Db	1681	ACTGATTAAGCATTTGGTAACTGTGACAGCAAGTTTACTCATATATACCTTAGATTGATTT 1740
QY	4869	AAAACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTTGAATACTCATGAC 4928
Db	1741	AAAACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTTGAATACTCATGAC 1800
QY	4929	CAAAATCCCTTAACGTCAGTTTCCTTCCACTGAGCGTCAGACCCCTAGAAAGATCA 4988
Db	1801	CAAAATCCCTTAACGTCAGTTTCCTTCCACTGAGCGTCAGACCCCTAGAAAGATCA 1860
QY	4989	AGGATCTTCTGAGATCCTTTTTCGCGGTAATCTGCTGCTTGAACAAACAAAAACC 5048
Db	1861	AGGATCTTCTGAGATCCTTTTTCGCGGTAATCTGCTGCTTGAACAAACAAAAACC 1920
QY	5049	ACCGCTACCGCGTGGTTTGGCGGATCAAGAGCTACAACTCTTTTTCGGAAGT 5108
Db	1921	ACCGCTACCGCGTGGTTTGGCGGATCAAGAGCTACAACTCTTTTTCGGAAGT 1980
QY	5109	AACTGGCTTACAGAGCGGATACCAAACTACTGCTCTTCTAGTGTAGCGCTAGTAGG 5168
Db	1981	AACTGGCTTACAGAGCGGATACCAAACTACTGCTCTTCTAGTGTAGCGCTAGTAGG 2040
QY	5169	CCAGCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCTGCTTAACTCTGTTACC 5228
Db	2041	CCAGCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCTGCTTAACTCTGTTACC 2100


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QY 5229 AGTGCGTCTGCGAGTGGCGATAGTCTGCTTACCGGGTTGACATCAAGACGATAGTT 5288
Db |||||
QY 2101 AGTGCGTCTGCGAGTGGCGATAGTCTGCTTACCGGGTTGACATCAAGACGATAGTT 2160
Db |||||
QY 5289 ACCGATAAGCGCGAGCGGTCGGCTGAACCGGGGGTTCGTGCACACAGCCAGCTTGGGA 5348
Db |||||
QY 2161 ACCGATAAGCGCGAGCGGTCGGCTGAACCGGGGGTTCGTGCACACAGCCAGCTTGGGA 2220
Db |||||
QY 5349 GCGAACGACCTACACCGAATCGATACCTACAGCGTGAGTATGAGAAAGCGCAGCTT 5408
Db |||||
QY 2221 GCGAACGACCTACACCGAATCGATACCTACAGCGTGAGTATGAGAAAGCGCAGCTT 2280
Db |||||
QY 5409 TCCCGAAGGAGAAAGCGGACGATATCGGTAAAGCGGAGGTTCGGAACAGGAGAGCG 5468
Db |||||
QY 2281 TCCCGAAGGAGAAAGCGGACGATATCGGTAAAGCGGAGGTTCGGAACAGGAGAGCG 2340
Db |||||
QY 5469 CACGAGGAGCTTCCAGGGGAAACGCTGCTATCTTTATAGTCTCTGCGGGTTTCGCCA 5528
Db |||||
QY 2341 CACGAGGAGCTTCCAGGGGAAACGCTGCTATCTTTATAGTCTCTGCGGGTTTCGCCA 2400
Db |||||
QY 5529 CCTCTGATGAGCGTGAATTTTGTGATGCTGTCAGGGGGGCGAGCCTATGGAAGAAA 5588
Db |||||
QY 2401 CCTCTGATGAGCGTGAATTTTGTGATGCTGTCAGGGGGGCGAGCCTATGGAAGAAA 2460
Db |||||
QY 5589 GCGCAGCAACGCGGCTTTTACGCTTCTGCGGCTTTTGTGCGCTTTTGTCTCATGTT 5648
Db |||||
QY 2461 GCGCAGCAACGCGGCTTTTACGCTTCTGCGGCTTTTGTGCGCTTTTGTCTCATGTT 2520
Db |||||
QY 5649 CTTTCTGCGTATCCCTGATTTCTGTGATAACCGTATTAACCGCTTTTGTGAGTGTGA 5708
Db |||||
QY 2521 CTTTCTGCGTATCCCTGATTTCTGTGATAACCGTATTAACCGCTTTTGTGAGTGTGA 2580
Db |||||
QY 5709 TACCGTCTGCGGAGCGGACGACGAGCGAGCGAGTCACTAGCGAGGAGCGGAGGA 5768
Db |||||
QY 2581 TACCGTCTGCGGAGCGGACGAGCGAGCGAGTCACTAGCGAGGAGCGGAGGA 2640
Db |||||
QY 5769 GCGCCCAATACGAAACCGCTCTCCCGCGGTTGCGCGATTCTATTAATGACG 5822
Db |||||
QY 2641 GCGCCCAATACGAAACCGCTCTCCCGCGGTTGCGCGATTCTATTAATGACG 2694
Db |||||

RESULT 13
ABK10687
ID ABK10687 standard; DNA; 9359 BP.
XX
AC ABK10687;
XX
DT 05-JUN-2002 (first entry)
XX
DE Transformation vector plasmid pVDH636 DNA.
XX
KW Grass; plant; transgenic; flowering inhibition; inflorescence; gene; ds;
KW tiller production; delayed heading; gibberellic acid; phytohormone; golf;
KW genetically modified grass; athletic field; sport; baseball; cricket;
KW football; rugby; soccer; tennis; lawn; landscaping; cattle; horse; sheep;
KW goat; animal feedstuff; Arabidopsis thaliana; Ath1; homeobox gene;
KW circular; cyclic; pVDH636.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 4930..6351
FT /*tag= a
FT /product= "Arabidopsis thaliana Ath1"
XX
PN WO200214486-A2.
XX
PD 21-FEB-2002.
XX
PF 16-AUG-2001; 2001WO-EP009570.
XX
PR 18-AUG-2000; 2000US-0226422P.
PR 27-NOV-2000; 2000US-0253274P.
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PR 27-NOV-2000; 2000US-0253274P.
PR 22-JUN-2001; 2001US-0300220P.
PA (ADVA-) ADVANTA SEEDS BV.
XX Van Der Valk P, Van Dun CMP, Smeekens SCM, Proveniers MCG;
XX WPI; 2002-257603/30.
XX P-PSDB; AAU76885.
XX
XX New genetically modified grass useful for growing and/or propagating
XX grass in athletic fields (for sports such as baseball, cricket, football,
XX golf, rugby, soccer and tennis), or as animal feedstuff for cattle, goat,
XX horse and sheep.
XX
XX Example 1; Fig 6; 45pp; English.
XX
XX The invention relates to a grass plant which has been genetically
XX modified to substantially inhibit generative propagation. The genetic
XX modification may result in a heritable change in one or more plant
XX characteristics such as inhibition of flowering (or substantial delay
XX that amounts to inhibition), absence of inflorescence, increased
XX production of tillers, delayed heading and inhibition of the
XX developmental switch from vegetative to generative growth. A method of
XX making a grass involves transforming the grass with a nucleic acid which
XX interferes with metabolism of gibberellic acid. A grass can be treated by
XX applying a phytohormone to at least partially relieve or reverse a change
XX in plant characteristic resulting from genetic modification. The
XX genetically modified grass is useful for growing and/or propagating grass
XX in athletic fields (for sports such as baseball, cricket, football, golf,
XX rugby, soccer and tennis) lawns, parks and other types of landscaping.
XX The grass is also useful as an animal feedstuff for cattle, goats, horses
XX and sheep, due to its increased vegetative growth, improved digestibility
XX and/or nutritional value as animal feedstuff. This sequence represents
XX plasmid pVDH636 DNA. This plasmid was used as a transformation vector for
XX production of transgenic grasses expressing the Arabidopsis thaliana
XX homeobox gene, Ath1
XX
XX Sequence 9359 BP; 2377 A; 2222 C; 2133 G; 2624 T; 0 U; 3 Other;
XX
XX Query Match 45.7%; Score 2658.4; DB 6; Length 9359;
XX Best Local Similarity 99.7%; Pred. No. 0;
XX Matches 2685; Conservative 0; Mismatches 6; Indels 3; Gaps 2;
XX
QY 3129 TCGGGCCCAATTCGCCCTATAGTCAGTCGATTAACAATTCACTGGCGCTGCTTTTACAC 3188
Db |||||
QY 4 TCGGGCCCAATTCGCCCTATAGTCAGTCGATTAACAATTCACTGGCGCTGCTTTTACAC 63
Db |||||
QY 3189 GTCGTGACTGGGAAAACCTTGGCGTTACCCAACTTAATCGCTTGCAGCACATCCCCCTT 3248
Db |||||
QY 64 GTCGTGACTGGGAAAACCTTGGCGTTACCCAACTTAATCGCTTGCAGCACATCCCCCTT 123
Db |||||
QY 3249 TCGCCAGCTGCGTAATAGCGAAGAGCGCCGACCGATCGCCCTTCCCAACAGTTGGCA 3308
Db |||||
QY 124 TCGCCAGCTGCGTAATAGCGAAGAGCGCCGACCGATCGCCCTTCCCAACAGTTGGCA 183
Db |||||
QY 3309 GCCTGAATGCGGAATGAGACGCGCCCTGTAGCGGGGCATTAAGCGCGGGGTGTGGT 3368
Db |||||
QY 184 GCCTGAATGCGGAATGAGACGCGCCCTGTAGCGGGGCATTAAGCGCGGGGTGTGGT 243
Db |||||
QY 3369 TACGCGCAGGTGACCGCTACACTTGCAGCGCCCTAGCGCCCTCTCTTCGTTTCTT 3428
Db |||||
QY 244 TACGCGCAGGTGACCGCTACACTTGCAGCGCCCTAGCGCCCTCTCTTCGTTTCTT 303
Db |||||
QY 3429 CCCTTCCTTTCTCGCCACGTTTCGCGGCTTTCCCGCTCAAGCTCTAAATCGGGGCTCCC 3488
Db |||||
QY 304 CCCTTCCTTTCTCGCCACGTTTCGCGGCTTTCCCGCTCAAGCTCTAAATCGGGGCTCCC 363
Db |||||
QY 3489 TTTAGGGTTCCGATTTAGCTTTACGCGACCTCGACGGCAAAAACCTTGATTTGGGTGA 3548
Db |||||
QY 364 TTTAGGGTTCCGATTTAGCTTTACGCGACCTCGACGGCAAAAACCTTGATTTGGGTGA 423
Db |||||
QY 3549 TGGTTACGCTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTC 3608
Db |||||
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QY 5769 GGGCCATACGCAACCGCTCTCCCGCGGTTGGCGGATTCATTATGCGAG 5822
 DB 2641 GGGCCATACGCAACCGCTCTCCCGCGGTTGGCGGATTCATTATGCGAG 2694

RESULT 14
 ID ADA41728/c
 ID ADA41728 standard; DNA; 3404 BP.
 XX ADA41728;
 XX 20-NOV-2003 (first entry)
 XX Plasmid pUJO-20 DNA.
 XX RNA-dependent RNA polymerase; RdRP; plant virus; amplification system;
 KW ds; circular; cyclic.
 XX Synthetic.
 XX WO2003014366-A2.
 XX 20-FEB-2003.
 XX 29-JUL-2002; 2002WO-DE002863.
 XX 30-JUL-2001; 2001DE-01037444.
 XX (PROB-) PROBIOGEN AG.
 XX Sandig V, Jordan I;
 XX WPI; 2003-248302/24.
 PT Amplifying nucleic acid in animal cells, useful e.g. for gene therapy or
 PT vaccination, uses an RNA-dependent, RNA-polymerase of a plant virus.
 XX

Example 2; Page 37-38; 39pp; German.

This invention describes a novel method for amplifying nucleic acid in animal cells by introducing an RNA-dependent RNA polymerase (RdRP) and its associated promoters and cis-acting signals from a plant virus into the cells. RdRP is normally active in plant cells and the gene that encodes it can be recovered from such cells. Both the RdRP and the promoter are from plant viruses, particularly turnip crinkle virus and the amplified RNA is a modified satellite or genomic RNA of this virus. The method is particularly used for amplification of RNA (which may be mRNA for protein synthesis; an effector, e.g. antisense RNA or ribozyme, or genomic RNA) in animal cells, for (i) control of gene expression or (ii) for gene therapy or vaccination. When the system includes an inducible promoter, it permits strong and rapid expression of reporter genes in response to a test substance, especially where the promoter responds to the human immune deficiency virus or heavy metals, to produce a diagnostic system or biosensor, respectively. The method of the invention provides an inducible or constitutive, autonomous RNA-dependent RNA amplification system for animal cells that requires only one polymerase and does not use any viral structural genes or helper viruses. Amplification takes place in the cytoplasm without using any components potentially infectious for the host cells. Human 293 cells were transformed with (i) pUJO-39, expressing a turnip crinkle virus 88 kD protein; (ii) pUJO-60, expressed satellite RNA-C of the same virus in the sense orientation and a fusion of internal ribosome entry site and green fluorescent protein in the antisense orientation, and (iii) an expression vector for T7 RNA polymerase under control of the cytomegalovirus promoter. Expression of the reporter gene was detected by fluorescence microscopy. This sequence represents a fragment of plasmid, pUJO-20 DNA used in the invention.

Sequence 3404 BP; 858 A; 853 C; 863 G; 830 T; 0 U; 0 Other;

Query Match 45.4%; Score 2641.4; DB 8; Length 3404;
 Best Local Similarity 99.7%; Pred. No. 0;

Matches 2668; Conservative 0; Mismatches 6; Indels 3; Gaps 2;

QY 3146 TATAGTAGTGTATTAACAATTCATGCGCGTTCGTTTACAAACGTCGTGACATGGGAAAAAC 3205
 DB |||||
 3404 TATAGTAGTGTATTAACAATTCATGCGCGTTCGTTTACAAACGTCGTGACATGGGAAAAAC 3345
 QY |||||
 3206 CCTGGCGTTACCCAACTTAATCGCCTTCAGACACATCCCCCTTCGCCAGCTGGCGTAAT 3265
 DB |||||
 3344 CCTGGCGTTACCCAACTTAATCGCCTTCAGACACATCCCCCTTCGCCAGCTGGCGTAAT 3285
 QY |||||
 3266 AGCGAAGAGGCGCGCACCGATCGCCCTTCCCAACAGATTGCGCAGCTGAATGGCGAATGG 3325
 DB |||||
 3284 AGCGAAGAGGCGCGCACCGATCGCCCTTCCCAACAGATTGCGCAGCTGAATGGCGAATGG 3225
 QY |||||
 3326 AGCGCGCTGTAGCGCGCATTAAGCGCGGGGTGTGGTGTAGCGCAGCTGAACGCG 3385
 DB |||||
 3224 AGCGCGCTGTAGCGCGCATTAAGCGCGGGGTGTGGTGTAGCGCAGCTGAACGCG 3165
 QY |||||
 3386 CTACACTTGGCCAGCGCCTAGCGCGGCTCCCTTCGCTTCTTCCTTCTCTTCTTCGCCA 3445
 DB |||||
 3164 CTACACTTGGCCAGCGCCTAGCGCGGCTCCCTTCGCTTCTTCCTTCTCTTCTTCGCCA 3105
 QY |||||
 3446 CGTTCGCGGCTTCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTA 3505
 DB |||||
 3104 CGTTCGCGGCTTCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTA 3045
 QY |||||
 3506 GAGCTTTAGCGCAGCTCGACCGCAAAAACCTTGATTGGGTGATGGTTCACGTAGTGGGC 3565
 DB |||||
 3044 GTGCTTTACGGCACCTCGACCCCAAAAACCTTGATTGGGTGATGGTTCACGTAGTGGGC 2985
 QY |||||
 3566 CATGCGCCTGATAGACGGTTCCTCCCTTTGAGCTTGAGTTCACGCTCTTCTTAATAGTG 3625
 DB |||||
 2984 CATGCGCCTGATAGACGGTTCCTCCCTTTGAGCTTGAGTTCACGCTCTTCTTAATAGTG 2925
 QY |||||
 3626 GACTCTTCTTCAAACTGGAACAACTCAACCTTATCTCGTCTATCTTCTTTGATTAT 3685
 DB |||||
 2924 GACTCTTCTTCAAACTGGAACAACTCAACCTTATCTCGTCTATCTTCTTTGATTAT 2865
 QY |||||
 3686 AAGGATTTTCCGATTTCCGCTTATGTTTAAATAATGAGCTGATTTTAAACAAATTTTA 3745
 DB |||||
 2864 AAGGATTTTCCGATTTCCGCTTATGTTTAAATAATGAGCTGATTTTAAACAAATAATTA 2805
 QY |||||
 3746 ACGGAAATTTTAAACAAATATTAAGTTTACAAATTCCTCGTATGCGGTATTTCTCCTT 3805
 DB |||||
 2804 ACGGAAATTTTAAACAAATATTAAGCTTACAAATTT--CCTGATCGGTATTTCTCCTT 2747
 QY |||||
 3806 ACGCATCTGTGGGTATTTACACCGCATACAGGTGGCACTTTTCGGGGAATGTGGCGG 3865
 DB |||||
 2746 ACGCATCTGTGGGTATTTACACCGCAT--CAGGTGGCACTTTTCGGGGAATGTGGCGG 2688
 QY |||||
 3866 GAACCCCTATTTGTTTATTTTCTTAAATACATTCAAATATGATATCCGCTCATGACAAAT 3925
 DB |||||
 2687 GAACCCCTATTTGTTTATTTTCTTAAATACATTCAAATATGATATCCGCTCATGACAAAT 2628
 QY |||||
 3926 AACCTGATAATGCTTCAATAATTAACAAAGAGAGATGATGATTTTCAACATTTCC 3985
 DB |||||
 2627 AACCTGATAATGCTTCAATAATTAACAAAGAGAGATGATGATTTTCAACATTTCC 2568
 QY |||||
 3986 GTGTCGCCCTTATTTCCCTTTTTCGGCATTTTTCCTTCTCTGTTTTCCTCACCAGAAA 4045
 DB |||||
 2567 GTGTCGCCCTTATTTCCCTTTTTCGGCATTTTTCCTTCTCTGTTTTCCTCACCAGAAA 2508
 QY |||||
 4046 CGCTGGTGAAGTAAAGATGCTGAAGATCAGTTGGGTGACAGAGTGGGTATACATCGAAC 4105
 DB |||||
 2507 CGCTGGTGAAGTAAAGATGCTGAAGATCAGTTGGGTGACAGAGTGGGTATACATCGAAC 2448
 QY |||||
 4106 TGGATCTCAACAGCGGTAAAGATCCTTGAGGTTCGCCCCCGAAGAGCTTTTCCAATGA 4165
 DB |||||
 2447 TGGATCTCAACAGCGGTAAAGATCCTTGAGGTTCGCCCCCGAAGAGCTTTTCCAATGA 2388
 QY |||||
 4166 TGAGCAGCTTTTAAAGTTCTGCTATGTGGCGGGTATTATCCGCTATTTGACCGCGGGAAG 4225
 DB |||||
 2387 TGAGCAGCTTTTAAAGTTCTGCTATGTGGCGGGTATTATCCGCTATTTGACCGCGGGAAG 2328

XX
PS
XX
CC The invention relates to a construct which allows animals to be bred in
CC captivity but renders them infertile in the wild by allowing reversible
CC control over fertility and reproduction. The construct comprises a native
CC promoter, a blocking DNA sequence contoured for and designed to abrogate
CC a crucial gene's function or to cause its mis-expression, and a genetic
CC switch to regulate controlled expression/repression of the blocker/gene
CC knockout. The construct is useful for preventing embryogenesis or
CC gametogenesis in animals by stably transforming an animal cell with the
CC construct by microinjection, transfection or infection, where the
CC construct stably integrates into the genome by homologous recombination,
CC and implanting the cell into a host organism, where a whole animal
CC develops from the implanted cell. The present DNA sequence is plasmid
CC construct pHSP70-1MCS used for transfection of Pacific oysters. The
CC plasmid contains Drosophila heat shock promoter 70 (dHSP70) and its poly
CC adenylation signal

XX
SO Sequence 3968 BP: 1075 A; 917 C; 943 G; 1033 T; 0 U; 0 Other;

Qy	3907	TATCCGCTCATGAGACAATAACCTTGATAAATGCTTCAATAATTAATTGAAAAAGGAGAGT	3966
Db	3248	TATCCGCTCATGAGACAATAACCTTGATAAATGCTTCAATAATTAATTGAAAAAGGAGAGT	3189
Qy	3967	ATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTCGGGCATTTTGCCTTCCT	4026
Db	3188	ATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTCGGGCATTTTGCCTTCCT	3129
Qy	4027	GTTTTTTGCTCACCCAGAAACGCTGGTGAAGTAAAAAGATGCTGAAAGATCAGTTGGGTGCA	4086
Db	3128	GTTTTTTGCTCACCCAGAAACGCTGGTGAAGTAAAAAGATGCTGAAAGATCAGTTGGGTGCA	3069
Qy	4087	CGAGTGGGTTCATTCGAATCGGATCTCAACAGCGGTAAAGATCCTTGAGAGTTTTTCGCC	4146
Db	3068	CGAGTGGGTTCATTCGAATCGGATCTCAACAGCGGTAAAGATCCTTGAGAGTTTTTCGCC	3009
Qy	4147	GAAGAACGTTTTCCAAATGATGACACATTTTAAAGTTCTGCTATGTGGCGGCTATTATCC	4206
Db	3008	GAAGAACGTTTTCCAAATGATGACACATTTTAAAGTTCTGCTATGTGGCGGCTATTATCC	2949
Qy	4207	CGTATTGACCGCGGCAAGACAACTCGGTGCGCGATACACTATTCTCAGAATGACTTG	4266
Db	2948	CGTATTGACCGCGGCAAGACAACTCGGTGCGCGATACACTATTCTCAGAATGACTTG	2889
Qy	4267	GTTGAGTATCTACAGTCTACAGAAAAGCATCTTACCGATGGCATGACAGTAAAGAAATTA	4326
Db	2888	GTTGAGTATCTACAGTCTACAGAAAAGCATCTTACCGATGGCATGACAGTAAAGAAATTA	2829
Qy	4327	TGCAGTGTCTCCATACCATGAGTGATTAACACTGCGGCCCACTTACTTCTGACAAACGATC	4386
Db	2828	TGCAGTGTCTCCATACCATGAGTGATTAACACTGCGGCCCACTTACTTCTGACAAACGATC	2769
Qy	4387	GGAGGACCGAAGGAGCTAAACCGCTTTTTTGCACAACATGGGGGATCATGTAACTCGCCTT	4446
Db	2768	GGAGGACCGAAGGAGCTAAACCGCTTTTTTGCACAACATGGGGGATCATGTAACTCGCCTT	2709
Qy	4447	GATCGTTGGGAAACCGGAGCTGAATGAAAGCATATCCAAAACGAGCGGTGACACACGATG	4506
Db	2708	GATCGTTGGGAAACCGGAGCTGAATGAAAGCATATCCAAAACGAGCGGTGACACACGATG	2649
Qy	4507	CCGTAGCAATGCACACACGTTTGGCCAACTATTAACTGGCGCACTTACTTACTCTAGCT	4566
Db	2648	CCGTAGCAATGCACACACGTTTGGCCAACTATTAACTGGCGCACTTACTTACTCTAGCT	2589
Qy	4567	TCCCGGCACAAATTAATAGACTGGATGGAGCGCGATAAAGTTGCGAGACCACCTTCTCGCG	4626
Db	2588	TCCCGGCACAAATTAATAGACTGGATGGAGCGCGATAAAGTTGCGAGACCACCTTCTCGCG	2529
Qy	4627	TCGGCCCTTCGGCTGGCTGGTTATTGCTGATAAAATCTCGAGCCGCTGAGCGTGGGTCT	4686
Db	2528	TCGGCCCTTCGGCTGGCTGGTTATTGCTGATAAAATCTCGAGCCGCTGAGCGTGGGTCT	2469
Qy	4687	CGCGGTATCATTCAGCACCTGGGCGCCAGATGGTAAGCCCTCCCGATTCGTAAGTTATCTAC	4746
Db	2468	CGCGGTATCATTCAGCACCTGGGCGCCAGATGGTAAGCCCTCCCGATTCGTAAGTTATCTAC	2409
Qy	4747	ACGACGGGAGTCAGGCACATATGATGATGAACGAATAAGACAGATCGCTGAGATAGGTGCC	4806
Db	2408	ACGACGGGAGTCAGGCACATATGATGATGAACGAATAAGACAGATCGCTGAGATAGGTGCC	2349
Qy	4807	TCACTGATTAAAGCATTGGTAACCTGCAGACCAAGTTTACTCATATATACATTTAGATTGAT	4866
Db	2348	TCACTGATTAAAGCATTGGTAACCTGCAGACCAAGTTTACTCATATATACATTTAGATTGAT	2289
Qy	4867	TTAAAACTTCATTTTAAATTTAAAGATCTAGTGAAGATCCTTTTGTGATATCTCATG	4926
Db	2288	TTAAAACTTCATTTTAAATTTAAAGATCTAGTGAAGATCCTTTTGTGATATCTCATG	2229
Qy	4927	ACCAAAATCCCTTAAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAAGATC	4986
Db	2228	ACCAAAATCCCTTAAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAAGATC	2169
Qy	4987	AAAGGATCTCTTTGAGATCCCTTTTTTCTGCGCGGCTAATCTGCTGCTTGCACAAACAAAAA	5046

Db	2168	AAAGGATCTTTCTTGAGATCCCTTTTCTCGCGTAACTCTGCTTTGCAACAAAAA	2109
QY	5047	CCACCGGTACAGCGGTGGTTTTCGCCGATCAAGAGCTACCAACTCTTTTTCGGAAG	5106
Db	2108	CCACCGGTACAGCGGTGGTTTTCGCCGATCAAGAGCTACCAACTCTTTTTCGGAAG	2049
QY	5107	GTAACTGGCTTACAGAGCGCAGATACCAAACTCTCTCTCTAGTAGCCGTAGTTA	5166
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2755.6	47.3	5534	1	US-08-452-267-3
2	2755.6	47.3	5534	3	US-09-123-644-3
3	2630.4	45.2	3485	4	US-08-939-366-10
4	2553	43.9	4965	3	US-08-675-566-22
5	2553	43.9	5109	3	US-08-675-566-19
6	2553	43.9	6196	3	US-08-675-566-5
7	2553	43.9	6243	3	US-08-675-566-14
8	2553	43.9	6503	3	US-08-675-566-6
9	2553	43.9	6958	3	US-08-675-566-2
10	2553	43.9	7379	3	US-08-675-566-13
11	2553	43.9	8618	3	US-08-675-566-21
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43 2320 39.8 6714 1 US-08-021-623C-5 Sequence 5, Appli
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45 2313.8 39.7 6371 2 US-08-715-808-5 Sequence 5, Appli

ALIGNMENTS

RESULT 1
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; Sequence 3, Application US/08452267
; Patent No. 5801027
; GENERAL INFORMATION:
; APPLICANT: Bennett, Malcolm
; APPLICANT: May, Sean
; APPLICANT: Ramsey, Nichola
; TITLE OF INVENTION: Control of Genes in Transgenic Plants
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnes & Thornburg
; STREET: 11 South Meridian
; CITY: Indianapolis
; STATE: IN
; COUNTRY: USA
; ZIP: 46204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,267
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Breen, John P.
; REGISTRATION NUMBER: 38,833
; REFERENCE/DOCKET NUMBER: 6653-25744
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 231-7745
; TELEFAX: (317) 231-7433
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5534 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: PUMIGIT
; US-08-452-267-3

Query Match 47.3%; Score 2755.6; DB 1; Length 5534;
Best Local Similarity 96.3%; Pred. No. 0;
Matches 2890; Conservative 0; Mismatches 38; Indels 74; Gaps 4;


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RESULT 2

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; Sequence 3, Application US/09123644
; Patent No. 6127606
; GENERAL INFORMATION:
; APPLICANT: Bennett, Malcolm
; APPLICANT: May, Sean
; APPLICANT: Ramsay, Nicola
; TITLE OF INVENTION: Method of Using Transactivation Proteins to
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnes & Thornburg
; STREET: 11 South Meridian
; CITY: Indianapolis

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4051 CTAGCTTCCCGCAACAAATTAATAGACTGAGTGGCGGATAAAGTTGCGAGCACTT 4110
4621 CTGCGCTCGCCCTTCGCGTGGCTGTTTATTCGTGATAAATCTGAGCGCGTGAGCGT 4680
4111 CTGCGCTCGCCCTTCGCGTGGCTGTTTATTCGTGATAAATCTGAGCGCGTGAGCGT 4170
4681 GGTCTCGCGTATCATTCGAGCACTGGGCGCAGATGGTAAAGCCCTCCCGTATCGTAGTT 4740
4171 GGTCTCGCGTATCATTCGAGCACTGGGCGCAGATGGTAAAGCCCTCCCGTATCGTAGTT 4230
4741 ATCTACAGCGCGGAGTCAGGCAACTATGAGTGAACGAAATAGACAGATCGCTGAGATA 4800
4231 ATCTACAGCGCGGAGTCAGGCAACTATGAGTGAACGAAATAGACAGATCGCTGAGATA 4290
4801 GGTGCTCTCACTGATTAAGCACTGTAACCTGTCAGACCAAGTTTACTCATATATATCTTTAG 4860
4291 GGTGCTCTCACTGATTAAGCACTGTAACCTGTCAGACCAAGTTTACTCATATATATCTTTAG 4350
4861 ATTGATTTAAAACTTCAATTTTAAAGGATCTTAGTGAAGATCTTTTGTGATAAT 4920
4351 ATTGATTTAAAACTTCAATTTTAAAGGATCTTAGTGAAGATCTTTTGTGATAAT 4410
4921 CTATGACCAAAATCCCTTAACTGAGTTTTCGTTCCACTGAGCGTCAGACCCGTTAGAA 4980
4411 CTATGACCAAAATCCCTTAACTGAGTTTTCGTTCCACTGAGCGTCAGACCCGTTAGAA 4470
4981 AAGATCAAGAGTCTTCTGAGATCTTTTTCGCGCGTAACTCTGCTGCTTCAAAACA 5040
4471 AAGATCAAGAGTCTTCTGAGATCTTTTTCGCGCGTAACTCTGCTGCTTCAAAACA 4530
5041 AAAAAACACCGCTACACAGCGGTGTTGTTGCGGATCAAGAGTACCAACTCTTTTT 5100
4531 AAAAAACACCGCTACACAGCGGTGTTGTTGCGGATCAAGAGTACCAACTCTTTTT 4590
5101 CCGAAGGTAACTGCTTACAGAGCGCAGATACCAATACTGCTCTCTAGTCTAGCGG 5160
4591 CCGAAGGTAACTGCTTACAGAGCGCAGATACCAATACTGCTCTCTAGTCTAGCGG 4650
5161 TAGTTAGCCACCACTTCAAGAACTCTGTAGCAGCGCTCATACCTCGCTCTGCTAATC 5220
4651 TAGTTAGCCACCACTTCAAGAACTCTGTAGCAGCGCTCATACCTCGCTCTGCTAATC 4710
5221 CTGTTACAGTGGCTGCTGCGAGTGGCGATAAGTCTGTTCTTAACGGGTGGAATCAAGA 5280
4711 CTGTTACAGTGGCTGCTGCGAGTGGCGATAAGTCTGTTCTTAACGGGTGGAATCAAGA 4770
5281 CGATAGTTACCGGATAGGCGCAGCGTTCGGCTGAAACGGGGGTTCGTGACACAGCGCC 5340
4771 CGATAGTTACCGGATAGGCGCAGCGTTCGGCTGAAACGGGGGTTCGTGACACAGCGCC 4830
5341 AGCTTGAGCGGAAACGACCTACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGC 5400
4831 AGCTTGAGCGGAAACGACCTACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGC 4890
5401 GCCACGCTTCCGAGGAGGAAAGCGGACAGGTATCCGGTAAAGCGGAGCGGTGGAACA 5460
4891 GCCACGCTTCCGAGGAGGAAAGCGGACAGGTATCCGGTAAAGCGGAGCGGTGGAACA 4950
5461 GGAGAGCGCAGGAGGAGCTTCCAGGGGAAACCGCTGGTATCTTTATAGTCTCTCGG 5520
4951 GGAGAGCGCAGGAGGAGCTTCCAGGGGAAACCGCTGGTATCTTTATAGTCTCTCGG 5010
5521 TTTTCGCCACTCTGACTTGAAGTCTGATTTTGTGATGCTCTGTCAGGGGGCGGAGCCTA 5580
5011 TTTTCGCCACTCTGACTTGAAGTCTGATTTTGTGATGCTCTGTCAGGGGGCGGAGCCTA 5070

Qy	5581	TGGA	AAACGC	CAAGCA	CGGCGCTTTT	TACGTTCT	TGCGCTTTT	CTGCGCCTTTT	GTCT	5640
Db	5071	TGGA	AAACGC	CAAGCA	CGGCGCTTTT	TACGTTCT	TGCGCTTTT	CTGCGCCTTTT	GTCT	5130
Qy	5641	CACAT	GTCTT	CTCTCG	GTATCC	CTTGATTC	TGTAAC	CGTATTAC	CGGCTTTGAG	5700
Db	5131	CACAT	GTCTT	CTCTCG	GTATCC	CTTGATTC	TGTAAC	CGTATTAC	CGGCTTTGAG	5190
Qy	5701	TGAG	CTGATAC	CGGTC	CGCGAG	CCGCAAC	GACCGAG	CGCGAGT	CAGT	5760
Db	5191	TGAG	CTGATAC	CGGTC	CGCGAG	CCGCAAC	GACCGAG	CGCGAGT	CAGT	5250
Qy	5761	GCGA	AGAGCG	CCCAAT	ACGCAAC	CGCTCTCC	CGCGGTTG	CGCGATT	CA	5820
Db	5251	GCGA	AGAGCG	CCCAAT	ACGCAAC	CGCTCTCC	CGCGGTTG	CGCGATT	CA	5310
Qy	5821	AG	5822							
Db	5311	AG	5312							

RESULT 3

US-08-939-366-10/c
; Sequence 10, Application US/08939366
; Patent NO. 6355415
; GENERAL INFORMATION:
; APPLICANT: Wagner, Thomas E.
; APPLICANT: Xie, Yuesheng
; TITLE OF INVENTION: Compositions and Methods for the Use of
; TITLE OF INVENTION: Ribozymes to Determine Gene Function
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,366
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Carroll, Peter G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: OHU-02749
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3485 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-08-939-366-10

QY	3179	GTTTTACAACTCGTGA	CTGGGAAAA	CCCTGGCGGT	TTACCCAA	CTTAATCGCC	TTGAGCA	3239
Db	3258	G-TTTACAACTCGTGA	CTGGGAAAA	CCCTGGCGGT	TTACCCAA	CTTAATCGCC	TTGAGCA	3200
QY	3239	CATCCCCCTTTTCG	CAGCTGCGTAA	TAGCGAA	GAGGCGCG	CACCGAT	TAAAGCGCGCGG	3298
Db	3199	CATCCCCCTTTTCG	CAGCTGG-G	GTAA	TAGCGAA	GAGGCGCG	CACCGATGCGCCTTTCCCAA	3141
QY	3299	CAGTTGCGCAGCCT	GAATGGCGA	TGACGCGCCCT	GTAGCGGCGA	TAAAGCGCGCGG	3358	
Db	3140	CAGTTGCGCAGCCT	GAATGGCGA	TGACGCGCCCT	GTAGCGGCGA	TAAAGCGCGCGG	3081	
QY	3359	GTGTGTTGTTTAC	CGCGAGCGTGAC	CGCTTACA	CTTGC	CAGGCCC	TAGCGCGCTTCCTT	3418
Db	3080	GTGTGTTGTTTAC	CGCGAGCGTGAC	CGCTTACA	CTTGC	CAGGCCC	TAGCGCGCTTCCTT	3021
QY	3419	TCGCTTTCTCCCT	TTCTCTCGCCAC	AGTTGCGCGCT	TTTCCCGCT	CTAGCTCT	TAAATC	3478
Db	3020	TCGCTTTCTCCCT	TTCTCTCGCCAC	AGTTGCGCGCT	TTTCCCGCT	CTAGCTCT	TAAATC	2966
QY	3479	GGGGGCTCCCTTT	AGGGTCCGAT	TTTAGAGCT	TTTAGCGCAC	CTTCGACCGCA	AAAAAACTTG	3538
Db	2960	GGGGGCTCCCTTT	AGGGTCCGAT	TTTAGAGCT	TTTAGCGCAC	CTTCGACCGCA	AAAAAACTTG	2901
QY	3539	ATTTGGGTGATG	TGTTTAC	AGTAGTGGG	CAATCGCCCT	GTATAGAC	GGTTTTTCGCGCCTTGA	3598
Db	2900	ATTTGGGTGATG	TGTTTAC	AGTAGTGGG	CAATCGCCCT	GTATAGAC	GGTTTTTCGCGCCTTGA	2841
QY	3599	CGTTGGAGTCCAC	GTCTTTTAA	TAGTGGA	CTCTTGT	TCCAACT	TGSAACAA	3658
Db	2840	CGTTGGAGTCCAC	GTCTTTTAA	TAGTGGA	CTCTTGT	TCCAACT	TGSAACAA	2781
QY	3659	CTATCTCGGTCT	ATTTCTTTTGA	TTTTAA	AGGGAATTTG	CGGATTTG	CGGCTATTTG	3718
Db	2780	CTATCTCGGTCT	ATTTCTTTTGA	TTTTAA	AGGGAATTTG	CGGATTTG	CGGCTATTTG	2721
QY	3719	AAATAGCTGATTA	TAAACAAAT	TTTAA	CGGAAATTTT	TAAACAAAT	TATTAACGGTTTACAA	3778
Db	2720	AAATAGCTGATTA	TAAACAAAT	TTTAA	CGGAAATTTT	TAAACAAAT	TATTAACGGTTTACAA	2661
QY	3779	TTTCGCTGATG	GGGTATTTT	CTCCTT	ACGATCTG	CGGGTATTT	CACCGCGATACAG	3838
Db	2660	TTTCGCTGATG	GGGTATTTT	CTCCTT	ACGATCTG	CGGGTATTT	CACCGCGATACAG	2601
QY	3839	GTGGCACTTTTCG	GGGAAATGTG	CGCGGAA	CCCTTATTT	TGTTTATTTT	CTTAAATACATT	3898
Db	2600	GTGGCACTTTTCG	GGGAAATGTG	CGCGGAA	CCCTTATTT	TGTTTATTTT	CTTAAATACATT	2541
QY	3899	CAAAATGTAT	CGCTCAT	GAGACAA	TAAACCC	TGATAAT	GCTTCAATAATTTGAAAA	3958
Db	2540	CAAAATGTAT	CGCTCAT	GAGACAA	TAAACCC	TGATAAT	GCTTCAATAATTTGAAAA	2481
QY	3959	GGAGAGTAT	GAGTATCA	CAATTTCC	GTGTCGCC	CTTATTC	CCCTTTTTTTCGGGCAATTTT	4018
Db	2480	GGAGAGTAT	GAGTATCA	CAATTTCC	GTGTCGCC	CTTATTC	CCCTTTTTTTCGGGCAATTTT	2421
QY	4019	GCCTTCCTGTTT	TGCTCACC	CAGAAA	CGCTG	GTAAGTAA	AGATGCTGAAGATCAGT	4078
Db	2420	GCCTTCCTGTTT	TGCTCACC	CAGAAA	CGCTG	GTAAGTAA	AGATGCTGAAGATCAGT	2361
QY	4079	TGGGTGCAC	GAGTGGGTT	TATCAT	CGAATGGAT	CTCAAC	CAGCGGTAAAGATCCTTCGAGGTT	4138
Db	2360	TGGGTGCAC	GAGTGGGTT	TATCAT	CGAATGGAT	CTCAAC	CAGCGGTAAAGATCCTTCGAGGTT	2301
QY	4139	TTGCCCCGAGAA	CGTTTTT	CCAATGAT	GAGCACT	TTTTTAA	AGTTCTGCTATGTGCGCGG	4198
Db	2300	TTGCCCCGAGAA	CGTTTTT	CCAATGAT	GAGCACT	TTTTTAA	AGTTCTGCTATGTGCGCGG	2241
QY	4199	TATTTATCC	CGTATG	ACGCGCGG	CAAGAC	TAATCGG	TCTTCTCAGA	4258
Db	2240	TATTTATCC	CGTATG	ACGCGCGG	CAAGAC	TAATCGG	TCTTCTCAGA	2181
QY	4259	ATGACTTGGT	TGAGTACT	CAC	CAGTCA	CAGAAA	AGCATCTTTACGGATGGCATGACATAA	4318

Db 2180 ATGACTTGGTTGAGTACTACCAAGTACAGAAAGCATCTTACCGATGGCATGACAGTAA 2121
QY GAGAAATATGCAAGTGTGCGATCAACATGATGATTAACATCTGCGGCAACTTACTTCTGA 4378
Db 2120 GAGAAATATGCAAGTGTGCGATCAACATGATGATTAACATCTGCGGCAACTTACTTCTGA 2061
QY CAACGATCGGAGGACGAGGAGTAAACCGCTTTTTCGCAACAACATGGGGGATCATGTAA 4438
Db 2060 CAACGATCGGAGGACGAGGAGTAAACCGCTTTTTCGCAACAACATGGGGGATCATGTAA 2001
QY CTGCGCTTGTATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAAACGACGAGCGTGACA 4498
Db 2000 CTGCGCTTGTATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAAACGACGAGCGTGACA 1941
QY CCACGATGCTGTAGCAATGGCAACAGCTTGGCAAACTATTAACTGGGGAATCTCTTA 4558
Db 1940 CCACGATGCTGTAGCAATGGCAACAGCTTGGCAAACTATTAACTGGGGAATCTCTTA 1881
QY CTCTAGCTTCCCGCAACAATTAATAGACTGGAGGCGGATAAAGTTGCAGGACCAAC 4618
Db 1880 CTCTAGCTTCCCGCAACAATTAATAGACTGGAGGCGGATAAAGTTGCAGGACCAAC 1821
QY TTCTGCGCTCGGCCCTTCCGCTCGCTGGTTTATTGCTGATAAATCTGAGCCCGGTGAGC 4678
Db 1820 TTCTGCGCTCGGCCCTTCCGCTCGCTGGTTTATTGCTGATAAATCTGAGCCCGGTGAGC 1761
QY GTGGGTCTCGCGGTATCATTTGACAGACTGGGGCCAGATGTTAAGCCCTCCGATCTGTAG 4738
Db 1760 GTGGGTCTCGCGGTATCATTTGACAGACTGGGGCCAGATGTTAAGCCCTCCGATCTGTAG 1701
QY TTATCTACACGACGGGAGTCAGGCACTATGAGTGAACGAAATAGACAGATCGCTGAGA 4798
Db 1700 TTATCTACACGACGGGAGTCAGGCACTATGAGTGAACGAAATAGACAGATCGCTGAGA 1641
QY TAGTGTGCTCTACTGATTAAGCAATGGTAAGTGTGAGCAACCAAGTTTACTCATATATCTTT 4858
Db 1640 TAGTGTGCTCTACTGATTAAGCAATGGTAAGTGTGAGCAACCAAGTTTACTCATATATCTTT 1581
QY AGATTGATTTAAACTTCAATTTTAAATTAAGGATAGTGAAGATCTCTTTTGA 4918
Db 1580 AGATTGATTTAAACTTCAATTTTAAATTAAGGATAGTGAAGATCTCTTTTGA 1521
QY ATCTCATGACCAAAATCCCTTAACTGAGTGTTCCTTCCACTGAGCGTCAGACCCGCTAG 4978
Db 1520 ATCTCATGACCAAAATCCCTTAACTGAGTGTTCCTTCCACTGAGCGTCAGACCCGCTAG 1461
QY AAAAGATCAAAAGGATCTTCTTGAATCCCTTTTTCGCGGTAAATCTGCTGCTTGGAAA 5038
Db 1460 AAAAGATCAAAAGGATCTTCTTGAATCCCTTTTTCGCGGTAAATCTGCTGCTTGGAAA 1401
QY CAAAAAACCCGCTACAGCGGTGTTTGTTCGCGGATCAAGAGCTACCACTCTTT 5098
Db 1400 CAAAAAACCCGCTACAGCGGTGTTTGTTCGCGGATCAAGAGCTACCACTCTTT 1341
QY TTCCGAAGTAACTGGCTTTCAGCAGCGCAGATACCAAACTCTCTCTCTAGTGTAGC 5158
Db 1340 TTCCGAAGTAACTGGCTTTCAGCAGCGCAGATACCAAACTCTCTCTCTAGTGTAGC 1281
QY CGTAGTTAGGCAACCACTTCAAGAACTCTGTAGCACCCTACATACCTCGCTCTGTAA 5218
Db 1280 CGTAGTTAGGCAACCACTTCAAGAACTCTGTAGCACCCTACATACCTCGCTCTGTAA 1221
QY TCCTGTTACAGTGTGCTGCTGAGTGGGATGATGCTGCTTACCGGTTGGACTCAA 5278
Db 1220 TCCTGTTACAGTGTGCTGCTGAGTGGGATGATGCTGCTTACCGGTTGGACTCAA 1161
QY GACGATAGTTACCGGATAGGCGCAGCGTCCGCTGAAACCGGGGTTCTGTGACACAGC 5338
Db 1160 GACGATAGTTACCGGATAGGCGCAGCGTCCGCTGAAACCGGGGTTCTGTGACACAGC 1101
QY CCAGCTTGGAGGAAACGACCTACACGGAAGTACGATACCTACAGGCTGAGCTATGAGAA 5398

Db 1100 CCAGCTTGGAGCGAAGCACTACACGAACTGAGATACCTACAGCGTGAGCTATGAGAAA 1041
QY GCCCCACGCTTCCGGAAGGAGGAGGCGGACAGGTTATCCGGTAAGCGGCGAGGTCGGAA 5458
Db 1040 GCCCCACGCTTCCGGAAGGAGGAGGCGGACAGGTTATCCGGTAAGCGGCGAGGTCGGAA 981
QY CAGGAGGCGCACGAGGAGCTTCCAGGGGGAACCGCTGGTATCTTTATAGTCTCTCG 5518
Db 980 CAGGAGGCGCACGAGGAGCTTCCAGGGGGAACCGCTGGTATCTTTATAGTCTCTCG 921
QY GGTTCGCCACCTCTGACTTGGCTGATTTTGTGATGCTGCTCAGGGGGGCGGAGCC 5578
Db 920 GGTTCGCCACCTCTGACTTGGCTGATTTTGTGATGCTGCTCAGGGGGGCGGAGCC 861
QY TATGGAACAAACGCGCAGCAACCGCTTTTACGGTTCCTGGCTTTTGTGCTGGCTTTT 5638
Db 860 TATGGAACAAACGCGCAGCAACCGCTTTTACGGTTCCTGGCTTTTGTGCTGGCTTTT 801
QY CTCACATGTTTCTTCTGCGTTATCCCTGATCTGCTGATTAACCGTATTACCGCTTTT 5698
Db 800 CTCACATGTTTCTTCTGCGTTATCCCTGATCTGCTGATTAACCGTATTACCGCTTTT 741
QY AGTGAGCTGATACCGCTCGCGCAGCGCAACCGCAGCGCAGCGAGTCACTGAGCGAGG 5758
Db 740 AGTGAGCTGATACCGCTCGCGCAGCGCAACCGCAGCGCAGCGAGTCACTGAGCGAGG 681
QY AAGCGGAAGAGCGCCCAATACGCAACCGCTCTTCCCGCGCGCTTCCCGCGCTTCAATTAAT 5818
Db 680 AAGCGGAAGAGCGCCCAATACGCAACCGCTCTTCCCGCGCGCTTCCCGCGCTTCAATTAAT 621
QY 5819 GCAG 5822
Db 620 GCAG 617

RESULT 4

US-08-675-566-22/c
; Sequence 22, Application US/08675566
; Patent No. 6090393
; GENERAL INFORMATION:
; APPLICANT: Fischer, Laurent
; TITLE OF INVENTION: PROMOTERS, EXPRESSION CASSETTES,
; TITLE OF INVENTION: RECOMBINANT VIRUSES, METHODS FOR MAKING, AND USES THEREOF
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,566
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer Esq., William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2890
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)840-3333
; TELEFAX: (212)840-0712
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4965 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)									
US-08-675-566-22									
Query Match 43.9%; Score 2553; DB 3; Length 4965;									
Best Local Similarity 97.7%; Pred. No. 0;									
Matches 2632; Conservative 0; Mismatches 5; Indels 56; Gaps 2;									
QY	3134	CCCAATTCGCCCTATAGTGTAGTGTGCTATTACAAATTCACGTGCCGCTCGTTTACAAAGTCGT	3193						
DB	4922	CCCAATTCGCCCTATAGTGTAGTGTGCTATTACAAATTCACGTGCCGCTCGTTTACAAAGTCGT	4863						
QY	3194	GACTGGGAAACCCCTGGCGTTACCCAACTTAATTCGCTTGCACACATCCCTTCGCC	3253						
DB	4862	GACTGGGAAACCCCTGGCGTTACCCAACTTAATTCGCTTGCACACATCCCTTCGCC	4803						
QY	3254	AGCTGCGCTAATAGCAAGAGGCGCCGACCGATTCGCTTCCCAACAGTTGCGACGCTG	3313						
DB	4802	AGCTGCGCTAATAGCAAGAGGCGCCGACCGATTCGCTTCCCAACAGTTGCGACGCTG	4743						
QY	3314	AATGGCGAATG-----GACGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGGTGT	3369						
DB	4742	AATGGCGAATGCGCGACGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGGTGT	4683						
QY	3370	ACGCGAGCGTGACCGCTACCTGTCGCGCCCTAGCGCCCTTCCCTTCGCTTCTTC	3429						
DB	4682	ACGCGAGCGTGACCGCTACCTGTCGCGCCCTAGCGCCCTTCCCTTCGCTTCTTC	4623						
QY	3430	CTTCTCTTCTCGCGCACTTCGCGGCTTCCCGCTCAAGCTCTAAATCGGGGCTCCCT	3489						
DB	4622	CTTCTCTTCTCGCGCACTTCGCGGCTTCCCGCTCAAGCTCTAAATCGGGGCTCCCT	4563						
QY	3490	TTAGGGTTCCGATTTAGAGCTTTACGGCACCTCGACCGCAAAACCTTGATTTGGTGAT	3549						
DB	4562	TTAGGGTTCCGATTTAGAGCTTTACGGCACCTCGACCGCAAAACCTTGATTTGGTGAT	4503						
QY	3550	GGTTACGTAAGTGGCCATCGCCCTGATAGACGGTTTTCGCCCTTTGACGTTGAGTCC	3609						
DB	4502	GGTTACGTAAGTGGCCATCGCCCTGATAGACGGTTTTCGCCCTTTGACGTTGAGTCC	4443						
QY	3610	AGTTCTTTTAAAGTGGATCTTGTTCGCGCTATTGCTTAAATAATCAGCTG	3669						
DB	4442	AGTTCTTTTAAAGTGGATCTTGTTCGCGCTATTGCTTAAATAATCAGCTG	4383						
QY	3670	TATCTTTTGTATTAAGGGATTTTCGCGATTTTCGCGCTATTGCTTAAATAATCAGCTG	3729						
DB	4382	TATCTTTTGTATTAAGGGATTTTCGCGATTTTCGCGCTATTGCTTAAATAATCAGCTG	4323						
QY	3730	ATTTAACAAATTTTAAACCGGAATTTTAAACAAATTTTAAACAAATTTTAAACAAATTTT	3789						
DB	4322	ATTTAACAAATTTTAAACCGGAATTTTAAACAAATTTTAAACAAATTTTAAACAAATTTT	4270						
QY	3790	CGGGTATTTTCTCTTACGCATCTGCGGTATTTTCACCGCATACAGGTGGCACTTTT	3849						
DB	4269	-----CCAGGTGGCACTTTT	4255						
QY	3850	CGGGAAATGTGCGGGAACCCCTATTGTTTATTTTCTAAATACATTCAAAATATGAT	3909						
DB	4254	CGGGAAATGTGCGGGAACCCCTATTGTTTATTTTCTAAATACATTCAAAATATGAT	4195						
QY	3910	CCGCTCATGACAAATACCCCTGATAAATGCTTCAATTAATTTGAAAAGGAAGATG	3969						
DB	4194	CCGCTCATGACAAATACCCCTGATAAATGCTTCAATTAATTTGAAAAGGAAGATG	4135						
QY	3970	AGTATTCAAATTTCCGCTGCGCCCTATTCCCTTTTTCGGGCAATTTTTCCTCTGTT	4029						
DB	4134	AGTATTCAAATTTCCGCTGCGCCCTATTCCCTTTTTCGGGCAATTTTTCCTCTGTT	4075						
QY	4030	TTTGTCTACCCAGAAACCGCTGTGAAGTAAAGATGCTGAAGATCAGTTGGGTGACGA	4089						
DB	4074	TTTGTCTACCCAGAAACCGCTGTGAAGTAAAGATGCTGAAGATCAGTTGGGTGACGA	4015						
QY	4090	GTGGGTATCATCGAACTGGATCTCAACAGCGGTAAAGATCCTTTGAGAGTTTTCGCCCGAA	4149						
DB		-----							
DB	4014	GTGGGTATCATCGAACTGGATCTCAACAGCGGTAAAGATCCTTGAGAGTTTTCGCCCGAA	3955						
QY	4150	GAACGTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGTGCGCGGTATTTATCCCGT	4209						
DB	3954	GAACGTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGTGCGCGGTATTTATCCCGT	3895						
QY	4210	ATTGAGCGCGGCAAGAGCAACTCGGTGCGCGCATACATTTCTCAGAAATGACTGGTT	4269						
DB	3894	ATTGAGCGCGGCAAGAGCAACTCGGTGCGCGCATACATTTCTCAGAAATGACTGGTT	3835						
QY	4270	GAGTACTCTACCACTACAGAAAAGCATCTTACGGATGGGATGACATTAAGAGATTTATGC	4329						
DB	3834	GAGTACTCTACCACTACAGAAAAGCATCTTACGGATGGGATGACATTAAGAGATTTATGC	3775						
QY	4330	AGTGTCTCCATTAACCATGATGATTAACACTGCGGCCAACTTACTCTGCAACGATCGGA	4389						
DB	3774	AGTGTCTCCATTAACCATGATGATTAACACTGCGGCCAACTTACTCTGCAACGATCGGA	3715						
QY	4390	GGACCGAAGGAGCTAACCGCTTTTGTGACACATCGGGGATCATGTAACTCGCCTTGAT	4449						
DB	3714	GGACCGAAGGAGCTAACCGCTTTTGTGACACATCGGGGATCATGTAACTCGCCTTGAT	3655						
QY	4450	CGTTGGAAACCGGAGCTGAATGAAGCATAACCAACGACGAGCGTGACACCGATGCCT	4509						
DB	3654	CGTTGGAAACCGGAGCTGAATGAAGCATAACCAACGACGAGCGTGACACCGATGCCT	3595						
QY	4510	GTAGCAATGGCAACACGTTGCGCAAACTTAACTGCGCAAACTTACTCTAGCTTCC	4569						
DB	3594	GTAGCAATGGCAACACGTTGCGCAAACTTAACTGCGCAAACTTACTCTAGCTTCC	3535						
QY	4570	CGGCAACAAATTAATAGACTGGAGCGGATTAAGTTGACGACCACTTCTGCGCTCG	4629						
DB	3534	CGGCAACAAATTAATAGACTGGAGCGGATTAAGTTGACGACCACTTCTGCGCTCG	3475						
QY	4630	GGCCTTCGCGCTGGCTTATCTGATTAATCTGATTAATCTGAGAGCGGTGAGCGTCTCG	4689						
DB	3474	GGCCTTCGCGCTGGCTTATCTGATTAATCTGATTAATCTGAGAGCGGTGAGCGTCTCG	3415						
QY	4690	GGTATCATTTGACGACTGGGCGCAGATGGTAAAGCCTTCCGCTATCGTAGTTATCTACAG	4749						
DB	3414	GGTATCATTTGACGACTGGGCGCAGATGGTAAAGCCTTCCGCTATCGTAGTTATCTACAG	3355						
QY	4750	ACGGGAGTCAAGGCACTATGATGAAGAAATAGACAGATCGCTGAGATAGTGCCTCA	4809						
DB	3354	ACGGGAGTCAAGGCACTATGATGAAGAAATAGACAGATCGCTGAGATAGTGCCTCA	3295						
QY	4810	CTGATTAAGCAATGCTAACTGTCAGACCAAGTTTACTCATATATATTTAGATTGATTA	4869						
DB	3294	CTGATTAAGCAATGCTAACTGTCAGACCAAGTTTACTCATATATATTTAGATTGATTA	3235						
QY	4870	AAACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTTGTAAATCTCATGACC	4929						
DB	3234	AAACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTTGTAAATCTCATGACC	3175						
QY	4930	AAAATCCCTTAACGTGAGTTTTCGTTCCAGTGGGTCAGACCCCGTAGAAAAGATCAA	4989						
DB	3174	AAAATCCCTTAACGTGAGTTTTCGTTCCAGTGGGTCAGACCCCGTAGAAAAGATCAA	3115						
QY	4990	GGATCTTCTTGAGATCCTTTTTCGCGCTAATCTGCTGCTTGCACCAAAAAACCA	5049						
DB	3114	GGATCTTCTTGAGATCCTTTTTCGCGCTAATCTGCTGCTTGCACCAAAAAACCA	3055						
QY	5050	CCGCTACAGCGGTGTTGTTGCGCGATCAAGAGTACCAACTCTTTTCCGAAGTA	5109						
DB	3054	CCGCTACAGCGGTGTTGTTGCGCGATCAAGAGTACCAACTCTTTTCCGAAGTA	2995						
QY	5110	ACTGGCTTACAGAGCGGATTAACAAATCTGCTTCTAGTGTAGCGTAGTTAGG	5169						
DB	2994	ACTGGCTTACAGAGCGGATTAACAAATCTGCTTCTAGTGTAGCGTAGTTAGG	2935						
QY	5170	CACCACTTCAAGAACTCTGTAGCACCGCTTACATACCTCGCTCTGCTTAATCTGTTACCA	5229						
DB	2934	CACCACTTCAAGAACTCTGTAGCACCGCTTACATACCTCGCTCTGCTTAATCTGTTACCA	2875						


```

; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer Esq., William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2890
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)840-3333
; TELEFAX: (212)840-0712
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6196 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-675-566-5

Query Match 43.9%; Score 2553; DB 3; Length 6196;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2632; Conservative 0; Mismatches 5; Indels 56; Gaps 2;

QY 3134 CCCAATTCGCCCTATAGTACGTCGTATTACAAATTCACCTGGCGCGTCGTTTACAAACGTCGT 3193
DB 6177 CCCAATTCGCCCTATAGTACGTCGTATTACAAATTCACCTGGCGCGTCGTTTACAAACGTCGT 6118

QY 3194 GACTGGGAAACCCCTGGCGTTTACCACACTTAATCGCCTTGCGACACATCCCCCTTTCGCC 3253
DB 6117 GACTGGGAAACCCCTGGCGTTTACCACACTTAATCGCCTTGCGACACATCCCCCTTTCGCC 6058

QY 3254 AGCTGGCGTAATAGCGAAGAGCGCGCACCGATCGCCCTTCCCAACAGTTGCGGAGCCTG 3313
DB 6057 AGCTGGCGTAATAGCGAAGAGAGCGCGCACCGATCGCCCTTCCCAACAGTTGCGGAGCCTG 5998

QY 3314 AATCGCGAATG ---GACGCGCCCTGTAGCGCGCATTTAAGCGCGGCGGTGTCGTGTT 3369
DB 5997 AATCGCGAATGCGCGAGCGCGCCCTGTAGCGCGCATTTAAGCGCGGCGGTGTCGTGTT 5938

QY 3370 ACGCGCAGCGTACCGGTACACTTGCACGCGCCCTAGCGCGCGCTCCTTTCGCTTTCCTC 3429
DB 5937 ACGCGCAGCGTACCGGTACACTTGCACGCGCCCTAGCGCGCGCTCCTTTCGCTTTCCTC 5878

QY 3430 CCTTCTCTTTCGCGCATGTTGCGCGCTTCCCGCTCAAGCTCTAAATCGGGGGTCCCT 3489
DB 5877 CCTTCTCTTTCGCGCATGTTGCGCGCTTCCCGCTCAAGCTCTAAATCGGGGGTCCCT 5818

QY 3490 TTAGGGTTCGATTTAGAGCTTTTACGCGACCTCGACCGCAAAACCTTGATTGGGTGAT 3549
DB 5817 TTAGGGTTCGATTTAGAGCTTTTACGCGACCTCGACCGCAAAACCTTGATTGGGTGAT 5758

QY 3550 GGTTCAGTGTGGGCCATCGCCCTGTAGACGCGTTCGCGCTTTCGCGCTTTCGAGTTC 3609
DB 5757 GGTTCAGTGTGGGCCATCGCCCTGTAGACGCGTTCGCGCTTTCGCGCTTTCGAGTTC 5698

QY 3610 ACGTCTTTTATAGTGGACTCTGTTCCAACTGGAACAAACACTCAACCTTATCTCGTC 3669
DB 5697 ACGTCTTTTATAGTGGACTCTGTTCCAACTGGAACAAACACTCAACCTTATCTCGTC 5638

QY 3670 TATCTTTTGTATTTAAGGATTTTTCGCGATTTTCGCGCTTATGTTTAAAAAATGAGCTG 3729
DB 5637 TATCTTTTGTATTTAAGGATTTTTCGCGATTTTCGCGCTTATGTTTAAAAAATGAGCTG 5578

QY 3730 ATTTAACAAATATTAAACGGAATTTTAAACAAATATTAAACGTTTACAAATTTTCGCTGAT 3789
DB 5577 ATTTAACAAATATTAAACGGAATTTTAAACAAATATTAAACGTTTACAAATTTTC 5525

QY 3790 GCGGTATTTCTCTTACGCACTCTGCGGTATTTCACACCGCATACAGGTGGCACTTTT 3849
DB 5524 -----CCAGGTGGCACTTTT 5510

QY 3850 CGGGAAATGTGCGGGAAACCCCTATTGTTTATTGTTTCTAAATACATTTCAAAATATGAT 3909
DB 5509 CGGGAAATGTGCGGGAAACCCCTATTGTTTATTGTTTCTAAATACATTTCAAAATATGAT 5450
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QY 3910 CCGCTCATGAGCAATAAACCCCTGATAAATGCTTCAATAAATATTGAAAAAGGAGATATG 3969
DB 5449 CCGCTCATGAGCAATAAACCCCTGATAAATGCTTCAATAAATATTGAAAAAGGAGATATG 5390

QY 3970 AGTATTCAACATTTCCGTCGCGCTTATCCCTTTTTCGGGCATTTTGCCTTCCTGTT 4029
DB 5389 AGTATTCAACATTTCCGTCGCGCTTATCCCTTTTTCGGGCATTTTGCCTTCCTGTT 5330

QY 4030 TTTGCTCACCCAGAAACCGTGGTGAAGTAAAGATGCTGAAGATCAGTTGGTGGTGCACGA 4089
DB 5329 TTTGCTCACCCAGAAACCGTGGTGAAGTAAAGATGCTGAAGATCAGTTGGTGGTGCACGA 5270

QY 4090 GTGGTTTACATCGAACTGGATCTCAACAGCGGTAAAGATCCTTGAAGATTTTTCGCCCGCAA 4149
DB 5269 GTGGTTTACATCGAACTGGATCTCAACAGCGGTAAAGATCCTTGAAGATTTTTCGCCCGCAA 5210

QY 4150 GAAAGTTTCCCAATGATGACACCTTTTAAAGTTCCTGCTATGTCGCGCGGTATTATCCCGT 4209
DB 5209 GAAAGTTTCCCAATGATGACACCTTTTAAAGTTCCTGCTATGTCGCGCGGTATTATCCCGT 5150

QY 4210 ATTGACCGCGGCAAGAGCAACTCGTTCGCGGCATACACTATTCTCAGAATGACTTGTT 4269
DB 5149 ATTGACCGCGGCAAGAGCAACTCGTTCGCGGCATACACTATTCTCAGAATGACTTGTT 5090

QY 4270 GAGTACTCACAGTCAAGAAAGCATCTTACCGATGGCATGACAGTAAGAGATTTATGC 4329
DB 5089 GAGTACTCACAGTCAAGAAAGCATCTTACCGATGGCATGACAGTAAGAGATTTATGC 5030

QY 4330 AGTCTGCCATACCATGATGATAACACTGCGGCCAACTTACTTCTGACAAACGATCGGA 4389
DB 5029 AGTCTGCCATACCATGATGATAACACTGCGGCCAACTTACTTCTGACAAACGATCGGA 4970

QY 4390 GGAACGGAAGAGCTAAACCGCTTTTTCGCAACAATGGGGGATCATGTAACCTCGCTTGAT 4449
DB 4969 GGAACGGAAGAGCTAAACCGCTTTTTCGCAACAATGGGGGATCATGTAACCTCGCTTGAT 4910

QY 4450 CGTTGGGAAACCGGAGCTGAATGAAGCCATACCAACGACGCGTGCACACCAAGTCC 4509
DB 4909 CGTTGGGAAACCGGAGCTGAATGAAGCCATACCAACGACGCGTGCACACCAAGTCC 4850

QY 4510 GTAGCAATGCAACAAACGTTGCGCAAACTATTAACTGCGCAACTTACTCTAGTCTCC 4569
DB 4849 GTAGCAATGCAACAAACGTTGCGCAAACTATTAACTGCGCAACTTACTCTAGTCTCC 4790

QY 4570 CGGCAACAAATTAATAGACTGGATGGAGCGGATAAAGTTGCAGAACCACTTCTCGCTCG 4629
DB 4789 CGGCAACAAATTAATAGACTGGATGGAGCGGATAAAGTTGCAGAACCACTTCTCGCTCG 4730

QY 4630 GCCCTTCGCGTGGCTGGTTTATTCCTGATTAATCTGGAGCCGGTGCAGCTGGGTCTCGC 4689
DB 4729 GCCCTTCGCGTGGCTGGTTTATTCCTGATTAATCTGGAGCCGGTGCAGCTGGGTCTCGC 4670

QY 4690 GGTATCATTTGAGCACTGGGCGCAGATGGTAAAGCCCTCCCGTATCTAGTATCTACACG 4749
DB 4669 GGTATCATTTGAGCACTGGGCGCAGATGGTAAAGCCCTCCCGTATCTAGTATCTACACG 4610

QY 4750 ACGGGAGTCAAGCAACTATGGATGAACGAAATAGACAGATCGCTGAGATAGGTGCCTCA 4809
DB 4609 ACGGGAGTCAAGCAACTATGGATGAACGAAATAGACAGATCGCTGAGATAGGTGCCTCA 4550

QY 4810 CTGATTAAAGCAATTTGGTAACTGTCAGACCAAGTTTACTCATATATACATTTAGATTGATTA 4869
DB 4549 CTGATTAAAGCAATTTGGTAACTGTCAGACCAAGTTTACTCATATATACATTTAGATTGATTA 4490

QY 4870 AAACTTCAATTTTAAATTTAAAGGATCTAGTGAAGATCCCTTTTGTAAATCTCATGACC 4929
DB 4489 AAACTTCAATTTTAAATTTAAAGGATCTAGTGAAGATCCCTTTTGTAAATCTCATGACC 4430

QY 4930 AAAATCCCTTAACTGAGTGTTCCTTCCACTGAGCGTCAGACCCCGCTGAGAAAGATCAAA 4989
DB 4429 AAAATCCCTTAACTGAGTGTTCCTTCCACTGAGCGTCAGACCCCGCTGAGAAAGATCAAA 4370

QY 4990 GGAATCTTCTGAGATCCCTTTTCTGCGCGTAACTCTGCTGCTTGCACAAACAAAAACCA 5049
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Db 4369 GGATCTCTTGGATCTCTTTTCTCGCGGTAATCTGCTGCTTGCACAAACAAAAACCA 4310
QY 5050 CCCTACCCAGCGTGGTTCTTTGCGCGGATCAAGAGCTACCACTCTTTTCCAGAGTA 5109
Db 4309 CCCTACCCAGCGTGGTTCTTTGCGCGGATCAAGAGCTACCACTCTTTTCCAGAGTA 4250
QY 5110 ACTGGCTTCAGCAGCGGATACCAATACTGTCTCTTCTAGTGAGCGGTAGTTAGGC 5169
Db 4249 ACTGGCTTCAGCAGCGGATACCAATACTGTCTCTTCTAGTGAGCGGTAGTTAGGC 4190
QY 5170 CACCACTTCAGAACTCTGTAGCAGCGCTACATACCTCTGCTCTGTCTTCTGTACCA 5229
Db 4189 CACCACTTCAGAACTCTGTAGCAGCGCTACATACCTCTGCTCTGTCTTCTGTACCA 4130
QY 5230 GTGGCTGTCCAGTCCGATAGTCTGTCTTACCGGTTGAGCTCAAGACATAGTTA 5289
Db 4129 GTGGCTGTCCAGTCCGATAGTCTGTCTTACCGGTTGAGCTCAAGACATAGTTA 4070
QY 5290 CCGGATAAGCGCGAGCGCTCGGCTGAAACCGGGGGTTCTGTGACACAGCCAGCTTGGAG 5349
Db 4069 CCGGATAAGCGCGAGCGCTCGGCTGAAACCGGGGGTTCTGTGACACAGCCAGCTTGGAG 4010
QY 5350 CGAAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCAGCTT 5409
Db 4009 CGAAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCAGCTT 3950
QY 5410 CCGGAAGCGAGAAAGCGGACAGGTATCCGGTAAAGCGGCGGAGGTGCGAAACAGGAGCGC 5469
Db 3949 CCGGAAGCGAGAAAGCGGACAGGTATCCGGTAAAGCGGCGGAGGTGCGAAACAGGAGCGC 3890
QY 5470 ACGAGGAGCTTCCAGGGGAAACGCTGTATCTTTATAGTCTCTCTCGGTTTCCGCCAC 5529
Db 3889 ACGAGGAGCTTCCAGGGGAAACGCTGTATCTTTATAGTCTCTCTCGGTTTCCGCCAC 3830
QY 5530 CTCTGACTGAGCTGATTTTGTGATCTCTGTAGGGGGGAGGCTATGAGAAAC 5589
Db 3829 CTCTGACTGAGCTGATTTTGTGATCTCTGTAGGGGGGAGGCTATGAGAAAC 3770
QY 5590 GCCAGCAGCGCGCTTTTACGGTCTCTCGGCTTTTGTGCGCTTTTGTGCGCTTTTGTGCGCT 5649
Db 3769 GCCAGCAGCGCGCTTTTACGGTCTCTCGGCTTTTGTGCGCTTTTGTGCGCTTTTGTGCGCT 3710
QY 5650 TTTCTGCTTATCCCTGATTTCTGTGGATAACCGTATTAACCGCTTTTGTGAGTGCTGAT 5709
Db 3709 TTTCTGCTTATCCCTGATTTCTGTGGATAACCGTATTAACCGCTTTTGTGAGTGCTGAT 3650
QY 5710 ACCGCTCGCGCAGCGCAACCGAGCGAGCTCAGTGAGGAGGAGGAGGAGGAG 5769
Db 3649 ACCGCTCGCGCAGCGCAACCGAGCGAGCTCAGTGAGGAGGAGGAGGAGGAG 3590
QY 5770 GSCCAATACGCAACCGCTCTCCCGCGGCTTTGCGCGATTCATTAATGCGAG 5822
Db 3589 GSCCAATACGCAACCGCTCTCCCGCGGCTTTGCGCGATTCATTAATGCGAG 3537
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RESULT 7

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US-08-675-566-14/c
; Sequence 14, Application US/08675566
; Patent No. 6090393
; GENERAL INFORMATION:
; APPLICANT: Fischer, Laurent
; TITLE OF INVENTION: PROMOTERS, EXPRESSION CASSETTES,
; TITLE OF INVENTION: RECOMBINANT VIRUSES, METHODS FOR MAKING, AND USES THEREOF
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,566
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer Esq., William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2890
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)840-3333
; TELEFAX: (212)840-0712
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6243 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-675-566-14
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Query Match 43.9%; Score 2553; DB 3; Length 6243;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2632; Conservative 0; Mismatches 5; Indels 56; Gaps 2;

QY 3134 CCCAATTCGCCCTATAGTGAAGTCTTACCAATTCACCTGCGCGTCTTTTACAACTCGT 3193
Db 6224 CCCAATTCGCCCTATAGTGAAGTCTTACCAATTCACCTGCGCGTCTTTTACAACTCGT 6165
QY 3194 GACTGGGAAAAACCTGGCGCTTACCAAACTTAATGCGCTTTCAGACACATCCCTTTTCGCC 3253
Db 6164 GACTGGGAAAAACCTGGCGCTTACCAAACTTAATGCGCTTTCAGACACATCCCTTTTCGCC 6105
QY 3254 AGCTGCGGTAATAGCGAAGAGCGCGCCAGCTGCGCTTCCCAACAGTTGGCAGCGCTG 3313
Db 6104 AGCTGCGGTAATAGCGAAGAGCGCGCCAGCTGCGCTTCCCAACAGTTGGCAGCGCTG 6045
QY 3314 AATGCGAATG---GAGCGCGCTTGTAGCGCGGATTAAGCGCGCGCGGTGCGTGGT 3369
Db 6044 AATGCGAATGCGCGGAGCGCGCTTGTAGCGCGGATTAAGCGCGCGCGGTGCGTGGT 5985
QY 3370 ACGCGAGCGTGACCGCTACACTTGCAGCGCTTGTAGCGCGCGCTTTCGCTTTCCTTC 3429
Db 5984 ACGCGAGCGTGACCGCTACACTTGCAGCGCTTGTAGCGCGCGCTTTCGCTTTCCTTC 5925
QY 3430 CTTTCTTTCTCGCGACGTTGCGCGCTTCCCGCTCAAGCTCTAAATCGGGGGCTCCCT 3489
Db 5924 CTTTCTTTCTCGCGACGTTGCGCGCTTCCCGCTCAAGCTCTAAATCGGGGGCTCCCT 5865
QY 3490 TTAGGGTTCCGATTTAGAGCTTTTACGGCACTTCGACCGCAAAACCTTGAATTTGGTGTAT 3549
Db 5864 TTAGGGTTCCGATTTAGAGCTTTTACGGCACTTCGACCGCAAAACCTTGAATTTGGTGTAT 5805
QY 3550 GTTTCAGCTAGTGGGCCATCGCCCTGTAGAGGTTTTTTCGCCCTTTTCAGCTTTCGAGTCC 3609
Db 5804 GTTTCAGCTAGTGGGCCATCGCCCTGTAGAGGTTTTTTCGCCCTTTTCAGCTTTCGAGTCC 5745
QY 3610 ACGTTCTTTATAGTGGACTCTTGTTCAAAACCTGGAACAACTCAACCTTATCTCGGTC 3669
Db 5744 ACGTTCTTTATAGTGGACTCTTGTTCAAAACCTGGAACAACTCAACCTTATCTCGGTC 5685
QY 3670 TATTCTTTTGTATTTATAGGATTTTTCGGCTTTCGGCTTTCGGCTTTCGGCTTTCGGCT 3729
Db 5684 TATTCTTTTGTATTTATAGGATTTTTCGGCTTTCGGCTTTCGGCTTTCGGCTTTCGGCT 5625
QY 3730 ATTTAACAAATATTAAACGCGAATTTTAAACAAATATTAAACGTTTTCGCTTTCGCTGAT 3789
Db 5624 ATTTAACAAATATTAAACGCGAATTTTAAACAAATATTAAACGTTTTCGCTTTCGCTGAT 5572
QY 3790 CGGTAATTTCTCTTACGCAATCTGTGCGGTATTTCACCGCATACAGGTGGCACTTTT 3849
```



```

/ ADDRESSEE: Curtis, Morris & Safford, P. C.
/ STREET: 530 Fifth Avenue
/ CITY: New York
/ STATE: New York
/ COUNTRY: United States of America
/ ZIP: 10036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/675,566
/ FILING DATE: 03-Jul-1996
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Frommer Esq., William S.
/ REGISTRATION NUMBER: 25,506
/ REFERENCE/DOCKET NUMBER: 454310-2890
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212)840-3333
/ TELEFAX: (212)840-0712
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6503 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-08-675-566-6

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Query Match	43.9%;	Score 2553;	DB 3;	Length 6503;
Best Local Similarity	97.7%;	Pred. No. 0;		
Matches 2632;	Conservative	0;	Mismatches	5;
			Indels	56;
			Gaps	2;
QY	3134	CCCAATTCGCCCTATAGTGGAGTCGTATTACAATTCACTGGCCGCGGTTTACAAACGTCGT	3193	
Db	6483			
QY	3194	GACTGGGAAACCCCTGGCGTTTACCACACTTAAATCGCTTCGAGACACATCCCCCTTTCGCC	3253	
Db	6423	GACTGGGAAACCCCTGGCGTTTACCACACTTAAATCGCTTCGAGACACATCCCCCTTTCGCC	6364	
QY	3254	AGCTGGCGTAAATAGCGAAGAGGCCGACCGATCGCCCTTCCCAACAGTTGCGCAGCGCTG	3313	
Db	6363	AGCTGGCGTAAATAGCGAAGAGGCCGACCGATCGCCCTTCCCAACAGTTGCGCAGCGCTG	6304	
QY	3314	AATGGCGAATG---GACGGCGCCCTGTAGGGCGCATTAAGCGGGCGGTTGTGGTGT	3369	
Db	6303	AATGGCGAATGGCGCGACGGCCCTGTAGGGCGCATTAAGCGGGCGGTTGTGGTGT	6244	
QY	3370	ACGCGACGCGTACCGCTACACTTGCAGCGCCCTAGCGCCGCTCCTTTCGCTTTCTTC	3429	
Db	6243	ACGCGACGCGTGACCGCTACACTTGCAGCGCCCTAGCGCCGCTCCTTTCGCTTTCTTC	6184	
QY	3430	CCTTCCTTTCTGCCACAGTTTCGCCGCTTCCCGCTCAAGCTCTAAATCGGGGCTCCCT	3489	
Db	6183	CCTTCCTTTCTGCCACAGTTTCGCCGCTTCCCGCTCAAGCTCTAAATCGGGGCTCCCT	6124	
QY	3490	TTAGGTTCCGATTTAGAGCTTTACGGCACTTCGCGGACGCGGACAAAACCTGATTTGGGTGAT	3549	
Db	6123	TTAGGTTCCGATTTAGTGTCTTTACGGCACTTCGCGGACGCGGACAAAACCTGATTTAGGGTGAT	6064	
QY	3550	GGTTACGTAAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTTGAGCTTTGGAGTCC	3609	
Db	6063	GGTTACGTAAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTTGAGCTTTGGAGTCC	6004	
QY	3610	ACGTTCTTTTAATAGTGGACTTTGTTCAAAACCTGGAACAACACTCAACCTATCTCGGTC	3669	
Db	6003	ACGTTCTTTTAATAGTGGACTTTGTTCAAAACCTGGAACAACACTCAACCTATCTCGGTC	5944	
QY	3670	TATTCCTTTGATTTATAAGGGAATTTGCCGATTTGCCGCTATTTGGTTAAAAAATGAGCTG	3729	

Db	5943	TATCTCTTTGATTATTAAGGGATTTTGGCGATTTCTGGGCTATTGTGTTAAAAAATGAGCTG	5894
Qy	3730	ATTATAACAATAATTTAAACCGGAATTTTAAACAAAATATTAAACGTTTACAAATTTTCGCCTGAT	3789
Db	5883	ATTATAACAATAATTTAAACCGGAATTTTAAACAAAATATTAAACGTTTACAAATTTTC-----	5831
Qy	3790	GGCGTATTTTCTCTTTCACGCACTCTGGCGGTATTTTACACGCGCATATAGGTGGCACTTTT	3849
Db	5830	-----CCAGGTGGCACTTTT	5816
Qy	3850	CGGGGAAATGTGGCGGACCCCTATTTTGTATTATTTTCTAAATACATTTCAAATATGATAT	3909
Db	5815	CGGGGAAATGTGGCGGAAACCCCTATTTTGTATTATTTTCTAAATACATTTCAAATATGATAT	5756
Qy	3910	CCGCTCATGAGACAATAACCCCTGATAAATGCTTCAATAATATTCGAAAGAGAGAGATG	3969
Db	5755	CCGCTCATGAGACAATAACCCCTGATAAATGCTTCAATAATATTCGAAAGAGAGAGATG	5696
Qy	3970	AGTATTCAACATTTCCGTGTGGCCCTTATCCCTTTTGTGGGCATTTTGCCTTCTCTGTT	4029
Db	5695	AGTATTCAACATTTCCGTGTGGCCCTTATCCCTTTTGTGGGCATTTTGCCTTCTCTGTT	5636
Qy	4030	TTTGTCTACCCAGAAACGCTGGTGAAGTAAAGATGCTGAAGATCAGTTGGGTGCACGA	4089
Db	5635	TTTGTCTACCCAGAAACGCTGGTGAAGTAAAGATGCTGAAGATCAGTTGGGTGCACGA	5576
Qy	4090	GTGGTTATCATCGAACTGGATCTCAACAGCGGTAAAGATCTTGAGAGTTTTCGCCCGGAA	4149
Db	5575	GTGGTTATCATCGAACTGGATCTCAACAGCGGTAAAGATCTTGAGAGTTTTCGCCCGGAA	5516
Qy	4150	GAACTGTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGGGTATTATCCCGT	4209
Db	5515	GAACTGTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGGGTATTATCCCGT	5456
Qy	4210	ATTGACGCGGCGAAGCACTCGGTGGCGGATACACTATTCTCAGATGATCTGGTT	4269
Db	5455	ATTGACGCGGCGAAGCACTCGGTGGCGGATACACTATTCTCAGATGATCTGGTT	5396
Qy	4270	GAGTACTCACCAGTCAACAGAAAACATCTTACGGATGGCATGACAGTAAAGAAATATCG	4329
Db	5395	GAGTACTCACCAGTCAACAGAAAGCATTTACCGATGGCATGACAGTAAAGAAATATCG	5336
Qy	4330	AGTGTCTGCATAACCATGAGTGATAACACTCGCGGCCAACTTACTCTGCAACAGATCGGA	4389
Db	5335	AGTGTCTGCATAACCATGAGTGATAACACTCGCGGCCAACTTACTCTGCAACAGATCGGA	5276
Qy	4390	GGACCGAAGGAGCTAACCGCTTTTGTGCACAAATGGGGATCATGTAATCGCTTGAT	4449
Db	5275	GGACCGAAGGAGCTAACCGCTTTTGTGCACAAATGGGGATCATGTAATCGCTTGAT	5216
Qy	4450	CGTTGGGAAACGGAGCTGAAATGAAGCCATACCAAAACGACGAGCGTGACACCAAGTGCCT	4509
Db	5215	CGTTGGGAAACGGAGCTGAAATGAAGCCATACCAAAACGACGAGCGTGACACCAAGTGCCT	5156
Qy	4510	GTACCAATGGCAACAACGTTTGGCCAAACTTATTAACCTGGCGAACTACTTACTAGCTTCC	4569
Db	5155	GTACCAATGGCAACAACGTTTGGCCAAACTTATTAACCTGGCGAACTACTTACTAGCTTCC	5096
Qy	4570	CGGCAACAATTAATAGACTGGATGGAGCGGATTAAGTTGCAGGACCACTTCTGGCGTCG	4629
Db	5095	CGGCAACAATTAATAGACTGGATGGAGCGGATTAAGTTGCAGGACCACTTCTGGCGTCG	5036
Qy	4630	GCCTTCCGCTGGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAAGTGGGTCTCGC	4689
Db	5035	GCCTTCCGCTGGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAAGTGGGTCTCGC	4976
Qy	4690	GGTATCATTTGCACACTGGGGCCAGATGTAAAGCCCTCCCGTATCGTAGTTATCTACACG	4749
Db	4975	GGTATCATTTGCACACTGGGGCCAGATGTAAAGCCCTCCCGTATCGTAGTTATCTACACG	4916
Qy	4750	ACGGGAGTCAAGCACTATGATGAAACGAATAGACAGATCGTGAGTAGGTGCTTCA	4809
Db	4915	ACGGGAGTCAAGCACTATGATGAAACGAATAGACAGATCGTGAGTAGGTGCTTCA	4856

QY 3610 ACCTTCTTTAATAGTGGACCTCTTGTTCCAAACCTGGAAACACTCAACCCCTATCTCGGTC 3669
DB |||||
QY 6458 ACCTTCTTTAATAGTGGACCTCTTGTTCCAAACCTGGAAACACTCAACCCCTATCTCGGTC 6399
DB |||||
QY 3670 TATCTCTTTGATTTATAAGGGATTTTGGCGATTTTCGGCCCTATTGGTTTAAAAATAGAGCTG 3729
DB |||||
QY 6398 TATCTCTTTGATTTATAAGGGATTTTGGCGATTTTCGGCCCTATTGGTTTAAAAATAGAGCTG 6339
DB |||||
QY 3730 ATTTAACAAATATTAAACGGGAATTTTAAACAAATATTAAAGTTTAAAGTTTTCGCCCTGAT 3789
DB |||||
QY 6338 ATTTAACAAATATTAAACGGGAATTTTAAACAAATATTAAAGTTTAAAGTTTTCGCCCTGAT 6286
DB |||||
QY 3790 GCGGTATTTCTCTTACGCATCTGTGCGGTATTTTACACCGCATACAGGTGGCACTTTT 3849
DB |||||
QY 6285 -----CCAGTGGCACTTTT 6271
DB |||||
QY 3850 CCGGGAATGTGCGGAAACCCCTATTGTGTTATTTTCTAAATACATTTCAATATGATAT 3909
DB |||||
QY 6270 CCGGGAATGTGCGGAAACCCCTATTGTGTTATTTTCTAAATACATTTCAATATGATAT 6211
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QY 3910 CCGCTCATGAGCAATAAACCCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGATATG 3969
DB |||||
QY 6210 CCGCTCATGAGCAATAAACCCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGATATG 6151
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QY 6150 AGTATTCAACATTTTCGTGTCGCCCTTATTCCCTTTTTCGGGCAATTTTGCCTTCTCGTT 6091
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QY 4030 TTTGCTCACCAGAAACCGTGTGAAAGTAAAGATGCTGAAGATCAGTTGGGTGCACGA 4089
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QY 4090 GTGGGTACATCGAATCGATCTAACAGCGGTAAAGATCCTTGAGAGTTTTCGCCCCGAA 4149
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QY 6030 GTGGGTACATCGAATCGATCTAACAGCGGTAAAGATCCTTGAGAGTTTTCGCCCCGAA 5971
DB |||||
QY 4150 GAAACGTTTTCGAATGAGCACTTTTAAAGTTCTGTATGTCGCGGTATTTATCCCGT 4209
DB |||||
QY 5970 GAAACGTTTTCGAATGAGCACTTTTAAAGTTCTGTATGTCGCGGTATTTATCCCGT 5911
DB |||||
QY 4210 ATTGACGCGGCAAGAGCAATCGGTGCGCGCATACACTATTCTCAGAATGACTTGGTT 4269
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QY 5910 ATTGACGCGGCAAGAGCAATCGGTGCGCGCATACACTATTCTCAGAATGACTTGGTT 5851
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QY 4270 GAGTACTCACCAGTCAACAGAAAGCATCTTACGATGGATGACATGACAGAAATATGTC 4329
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QY 5790 AGTGTGCGATAACCATGAGTGAATAACACTGCGGCGCACTTACTTCTGACACGATCGGA 5731
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QY 5670 GGTGGGAACCGGAGCTGAATGAAGCCATACCAACGAGAGCGGTGAACCAACGATGCT 5611
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QY 5550 CCGCAACAAATTAAGACTGGATGGAGCGGATAAAGTTGAGGACCACTTCTGCGCTCG 5491
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QY 5490 GCCCTTCGGCTGGCTGTTTATTGCTGATTAATCTGAGCGCGGTGAGCGTGGGTCTCGC 5431
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QY 4690 GGTATCATTCGACACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACAG 4749
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QY 4890 GTGGCTGTGCGCAGTGGCGATAGTCTGTCTTACCGGTTGAGCTCAAGACGATGTTA 4831
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QY 5290 CCGGATAAGGCGCAGCGTGGGCTGAAACGGGGGTCTGTGACACAGCCAGCTTGGAG 5349
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QY 4830 CCGGATAAGGCGCAGCGTGGGCTGAAACGGGGGTCTGTGACACAGCCAGCTTGGAG 4771
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QY 4770 GGAACGACTACACCGAACTGAGATACCTACAGCGTGTAGTATGAGAAAGCCGCTT 4711
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QY 4710 CCGGAAAGGAGAAAGGCGGACAGGTATCGGTAGCGGAGGTCGGAACAGGAGCGC 4651
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DB |||||
QY 4650 ACGAGGAGCTTCCAGGGGGAAACCGCTGTGTATCTTTATAGTCTGCTGGGTTTCGCCAC 4591
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QY 5530 CTCTGACTGTGCGTGTGATTTTGTGATGCTCGTCAGGGGGCGGAGCTTATGAAAAAC 5589
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QY 4590 CTCTGACTGTGCGTGTGATTTTGTGATGCTCGTCAGGGGGCGGAGCTTATGAAAAAC 4531
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QY 5590 GCGAGCAACGCGGCTTTTACGGTTCTTGCGCTTTTGTGCGCTTTTGTCTCAATGTC 5649
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QY 5650 TTTCTGCTTATCCCTGATTTCTGTGATTAACGTTATACCGCTTTTGTGAGTGTAT 5709
DB |||||
QY 4470 TTTCTGCTTATCCCTGATTTCTGTGATTAACGTTATACCGCTTTTGTGAGTGTAT 4411
DB |||||
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DB |||||
QY 4410 ACCGCTCGCGCAGCCGAAACGACCGAGCGAGTCAAGTGTGAGGAGGAGGAGGAG 4351
DB |||||
QY 5770 GCGCAATACGCAACCGCTCTCTCCCGCGGTTTGGCGGATTCATTAATGCGAG 5822
DB |||||

Db 4350 CGCCCAATACGAAACCGCTCTCCCGCGGTTGGCCGATTCATTAAATGACG 4298
|||||
RESULT 10
US-08-675-566-13/c
; Sequence 13, Application US/08675566
; Patent No. 6090393
; GENERAL INFORMATION:
; APPLICANT: Fischer, Laurent
; TITLE OF INVENTION: PROMOTERS, EXPRESSION CASSETTES,
; TITLE OF INVENTION: RECOMBINANT VIRUSES, METHODS FOR MAKING, AND USES THEREOF
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,566
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Prommer Esq., William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2890
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7379 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-675-566-13
Query Match 43.9%; Score 2553; DB 3; Length 7379;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2632; Conservative 0; Mismatches 5; Indels 56; Gaps 2;
QY 3134 CCCAATTCGCCCTATAGTAGAGTCGATTACAAATTCACATGGCGCGTCTTTTCAACAGTCGT 3193
Db 4265 CCCAATTCGCCCTATAGTAGAGTCGATTACAAATTCACATGGCGCGTCTTTTCAACAGTCGT 4206
QY 3194 GACTGGGAAACCCCTGGCGTTACCCAACTTAATGCGCTTGAGAGCAATCCCGCTTCGCC 3253
Db 4205 GACTGGGAAACCCCTGGCGTTACCCAACTTAATGCGCTTGAGAGCAATCCCGCTTCGCC 4146
QY 3254 AGCTGGCGTAATAGCGAAGAGCCCGCACCGATCGCCCTTCCCAACAGTTGGCGAGCCGTG 3313
Db 4145 AGCTGGCGTAATAGCGAAGAGCCCGCACCGATCGCCCTTCCCAACAGTTGGCGAGCCGTG 4086
QY 3314 AATGGCGAATG---GAGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGGTGT 3369
Db 4085 AATGGCGAATGCGGCGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGGTGT 4026
QY 3370 ACGCGCAGCGTGACCGCTACATTGCGAGCGCCCTAGCGCGCGCTTCCTTCGTTCTTC 3429
Db 4025 ACGCGCAGCGTGACCGCTACATTGCGAGCGCCCTAGCGCGCGCTTCCTTCGTTCTTC 3966
QY 3430 CCTTCCTTTCTCGCAGCTTCGCGGCTTTCCCGTCAAGCTCTAAATCGGGGCTCCCT 3489
Db 3965 CCTTCCTTTCTCGCAGCTTCGCGGCTTTCCCGTCAAGCTCTAAATCGGGGCTCCCT 3906

QY 3490 TTAGGGTTCCGATTTAGAGCTTTACGCACTCGACCGCAAAAACCTTGATTGGGTGAT 3549
Db 3905 TTAGGGTTCCGATTTAGTGTCTTTACGGCACCTCGACCCCAAAAACCTTGATTGGGTGAT 3846
QY 3550 GGTTCAGGTAGTGGGCCATCGCCCTGATAGACGGTTTTTTCGCCCTTTGACGTTGAGTCC 3609
Db 3845 GGTTCAGGTAGTGGGCCATCGCCCTGATAGACGGTTTTTTCGCCCTTTGACGTTGAGTCC 3786
QY 3610 ACGTTCTTTAATAGTGGACTCTTTGTTCCAAATCGAAACCAACACTCAACCCCTATCCGGTC 3669
Db 3785 ACGTTCTTTAATAGTGGACTCTTTGTTCCAAATCGAAACCAACACTCAACCCCTATCCGGTC 3726
QY 3670 TATCTTTTGAATTAAGGATTTTCCGATTTTCCGCTTATTCGTTTAAAAAAGTACGTC 3729
Db 3725 TATCTTTTGAATTAAGGATTTTCCGATTTTCCGCTTATTCGTTTAAAAAAGTACGTC 3666
QY 3730 ATTTAAACAATATTTTACGCGAATTTTAAACAAATATTTAAAGTTTACAAATTCGCTGAT 3789
Db 3665 ATTTAAACAATATTTTACGCGAATTTTAAACAAATATTTAAAGTTTACAAATTCGCTGAT 3613
QY 3790 GCGGTATTTCTCCTTACGCATCTGTGCGGTATTTTCAACGCGATACAGGTGGCACTTTT 3849
Db 3612 -----CCAGGTGGCACTTTT 3598
QY 3850 CGGGAAATGTGCGCGAAACCCCTATTGTTTATTTTCTTAATACATTTCAATATGTAT 3909
Db 3597 CGGGAAATGTGCGCGAAACCCCTATTGTTTATTTTCTTAATACATTTCAATATGTAT 3538
QY 3910 CCGCTCATGACACAATAACCCCTGATAATGCTTCAATAATATTGAAAAGGAAGAGTATG 3969
Db 3537 CCGCTCATGACACAATAACCCCTGATAATGCTTCAATAATATTGAAAAGGAAGAGTATG 3478
QY 3970 AGTATTCAACATTTCCGCTGTCGCCCTTATTTCCCTTTTTCGCGCATTTTTCCTCTGTT 4029
Db 3477 AGTATTCAACATTTCCGCTGTCGCCCTTATTTCCCTTTTTCGCGCATTTTTCCTCTGTT 3418
QY 4030 TTTGCTACCCAGAAACCGCTGTAAGTAAGTAAGTCTGAGTACAGTTCGGTGCACGA 4089
Db 3417 TTTGCTACCCAGAAACCGCTGTAAGTAAGTAAGTCTGAGATCAGTTGGTGACGA 3358
QY 4090 GTGGTTTACATCGAATCGATCTCAACAGCGGTAAAGTCTTGAAGTTTTCGCCCGCAA 4149
Db 3357 GTGGTTTACATCGAATCGATCTCAACAGCGGTAAAGTCTTGAAGTTTTCGCCCGCAA 3298
QY 4150 GAAAGTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGTGCGCGGTATTTATCCCGT 4209
Db 3297 GAAAGTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGTGCGCGGTATTTATCCCGT 3238
QY 4210 ATTGACGCGCGGAAGCAACTCGTTCGCCCATACACTATTCTCAGAAAGTACCTTGGT 4269
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QY 4270 GAGTACTCACAGTACAGAAAGCATCTTACGGATGGCATGACAGTAAGAAATATGTC 4329
Db 3177 GAGTACTCACAGTACAGAAAGCATCTTACGGATGGCATGACAGTAAGAAATATGTC 3118
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Db 3117 AGTGTGCGCATTAACCATGAGTGAATAACACTCGGCCAACTTACTTCTGACAGATCGGA 3058
QY 4390 GGAACGAGAGGACTAACCGCTTTTTCACAACATGGGGGATCATGTAACCTCGCTTGTAT 4449
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QY 4450 CTTTCGGGAACCGGAGCTGAATGAAGCCATACCAACGACGAGCGGTGACACCGATGCCT 4509
Db 2997 CTTTCGGGAACCGGAGCTGAATGAAGCCATACCAACGACGAGCGGTGACACCGATGCCT 2938
QY 4510 GTAGCAATGGCAACAAACGTTGCGAAATATTAACTGGGGAACCTACTTACTTAGCTTCC 4569
Db 2937 GTAGCAATGGCAACAAACGTTGCGAAATATTAACTGGGGAACCTACTTACTTAGCTTCC 2878
QY 4570 CGGCAACAATTAATAGACTGGATGGAGCGGATTAAGTTGACGAGCACTTCTTCGCTCG 4629

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Db      1797  TTTCCTGCGTTATCCCTGATTCTGTGGATAACCGTATTACCGCCTTTTGAGTGAGCTGAT 173
QY      5710  ACCGTCGCCGACGCGGAAACGACCGAGCGAGCGAGTCAGTGACGAGGAGCGGAAGAG 5769
Db      1737  ACCGTCGCCGACGCGGAAACGACCGAGCGAGCGAGTCAGTGACGAGGAGCGGAAGAG 1678
QY      5770  CGCCCAATACGCAAAACCGCTCTCCCGCGCGTTCGCCGATTCATTAAATGCAG 5822
Db      1677  CGCCCAATACGCAAAACCGCTCTCCCGCGCGTTCGCCGATTCATTAAATGCAG 1625

RESULT 11
US-08-675-566-21/c
; Sequence 21, Application US/08675566
; Patent No. 6090393
; GENERAL INFORMATION:
; APPLICANT: Fischer, Laurent
; TITLE OF INVENTION: PROMOTERS, EXPRESSION CASSETTES,
; TITLE OF INVENTION: RECOMBINANT VIRUSES, METHODS FOR MAKING, AND USES THEREOF
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,566
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer Esq., William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2890
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)840-3333
; TELEFAX: (212)840-0712
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8618 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-675-566-21

Query Match      43.9%; Score 2553; DB 3; Length 8618;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2632; Conservative 0; Mismatches 5; Indels 56; Gaps 2;

QY      3134  CCCAATTCGCCCTATAGTCAGTCGTATTACAATTCACTGGCCGTCGTTTACAAAGTCGT 3193
Db      8598  CCCAATTCGCCCTATAGTCAGTCGTATTACAATTCACTGGCCGTCGTTTACAAAGTCGT 8539
QY      3194  GACTGGGAAAAACCTGGCGTTTACCAACCTTAATCGCTTGCAGCACATCCCCCTTTCCGC 3253
Db      8538  GACTGGGAAAAACCTGGCGTTTACCAACCTTAATCGCTTGCAGCACATCCCCCTTTCCGC 8479
QY      3254  AGCTGCGTAATAGCGAAGAGCCCGCACCGTACGCGCTTCCCAACAGTTGGCGACGCTG 3313
Db      8478  AGCTGCGTAATAGCGAAGAGCCCGCACCGTACGCGCTTCCCAACAGTTGGCGACGCTG 8419
QY      3314  AATGGCGAATG-----GACGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGGTGTT 3369
Db      8418  AATGGCGAATGCGGACGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGGTGTT 8359
QY      3370  AGCGCAGCGTACGCGCTACACTTGCAGGCGCCCTAGCGCGCGCTTCCTTTTCGCTTTCTTC 3429

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Db	8358	ACGGCAGCGTGACGGCTACATCTGCCAGCGCCCTAGCGCGCTCCTTCGCTTCTTC	8299	7271
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Db	8298	CCCTCCCTTCTCGCCACGCTTCCCGCGCTTCCCGCTCAAGCTCTAAATCGGGGCTCCCT	8239	7211
Qy	3490	TTAGGGTTCCGATTTAGAGCTTTACGCGCCTCGACCGCAAAAACCTTGCTGGGTGAT	3549	4629
Db	8238	TTAGGGTTCCGATTTAGAGCTTTACGCGCCTCGACCGCAAAAACCTTGATAGGGTAT	8179	7151
Qy	3550	GGTTCAGCTAGTGGCCCATCGCCCTGATAGAGGTTTTTCCGCCCTTTGACGTTGAGTTC	3609	4689
Db	8178	GGTTCAGCTAGTGGCCCATCGCCCTGATAGAGGTTTTTCCGCCCTTTGACGTTGAGTTC	8119	7091
Qy	3610	ACGTTCTTTAATAGTGAGCTTCTGTTCCAACTCGAACCAACACTCAACCCCTATCTCGCTC	3669	4749
Db	8118	ACGTTCTTTAATAGTGAGCTTCTGTTCCAACTCGAACCAACACTCAACCCCTATCTCGCTC	8059	7031
Qy	3670	TATTTCTTTGATTTAAGGATTTTCCGATTTCCGCTATTGCTTAAATAATGAGCTG	3729	4809
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Qy	3730	ATTTTAACAAATTTTAAACGGAATTTTAAACAAATATTAAACGTTTACAAATTCGCTGAT	3789	4869
Db	7998	ATTTTAACAAATTTTAAACGGAATTTTAAACAAATATTAAACGTTTACAAATTCGCTGAT	7946	6911
Qy	3790	GCGGTATTTTCTCCTTACGCTATCTGCGGTATTTTCAACCGCATACAGGTGGCACTTTT	3849	4929
Db	7945	-----CCAGGTGGCACTTTT	7931	6851
Qy	3850	CGGGAAATGTGCGGGAACCCCTATTGTTTATTTTCTAAATACATTCAAAATATGAT	3909	4989
Db	7930	CGGGAAATGTGCGGGAACCCCTATTGTTTATTTTCTAAATACATTCAAAATATGAT	7871	6791
Qy	3910	CGCTCATGAGCAATAACCCCTGATTAATGCTTCAATAATATTGAAAAAGGAGTATG	3969	5049
Db	7870	CGCTCATGAGCAATAACCCCTGATTAATGCTTCAATAATATTGAAAAAGGAGTATG	7811	6731
Qy	3970	AGTATTTCAACATTTCCGCTGTCGCCCTTATCCCTTTTTCGGCATTTTGCCTTCTCTT	4029	5109
Db	7810	AGTATTTCAACATTTCCGCTGTCGCCCTTATCCCTTTTTCGGCATTTTGCCTTCTCTT	7751	6671
Qy	4030	TTTGCTCACCAAGAAACGCTGTGAAGTAAAGATGCTGAAGATCAGTTGGTGACGA	4089	5169
Db	7750	TTTGCTCACCAAGAAACGCTGTGAAGTAAAGATGCTGAAGATCAGTTGGTGACGA	7691	6611
Qy	4090	GTGGTTACATCGAATCTCAACAGCGGTAAAGATCCTTTGAGAGTTTTCGCCCGAA	4149	5229
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Qy	4210	ATTGACGCGGCAAGAGCACTCGGTCCGCCATACACTATTTCTCAGAATGACTTGGTT	4269	5349
Db	7570	ATTGACGCGGCAAGAGCACTCGGTCCGCCATACACTATTTCTCAGAATGACTTGGTT	7511	6431
Qy	4270	GAGTACTACCAAGTCAAGAAAAGCATCTTAAGGATGCGATGACAGTAAAGAAATTATGC	4329	5409
Db	7510	GAGTACTACCAAGTCAAGAAAAGCATCTTAAGGATGCGATGACAGTAAAGAAATTATGC	7451	6371
Qy	4330	AGTGTGCTCAACATGAGTCACTAACCTGCGGCCCACTTACTTCTGACACGATCGGA	4389	5469
Db	7450	AGTGTGCTCAACATGAGTCACTAACCTGCGGCCCACTTACTTCTGACACGATCGGA	7391	6311
Qy	4390	GGACCGAAGGAGTAAACCGCTTTTGTGCAACAATGGGGGATCATGTAACCTCGCTTGAT	4449	5529
Db	7390	GGACCGAAGGAGTAAACCGCTTTTGTGCAACAATGGGGGATCATGTAACCTCGCTTGAT	7331	6251
Qy	4450	CGTTGGGAACCGGAGCTGAATGAGCCATACCAACGACGAGGCTGACACGAGTGCCT	4509	6191

QY 5590 GCCAGCAACGGCGCTTTTACGGTTCCTGCGCTTTTCTGCGCTTTTGTGCTCATGTTTC 5649
Db 6190 GCCAGCAACGGCGCTTTTACGGTTCCTGCGCTTTTGTGCTCATGTTTC 6131
QY 5650 TTTCTCGGTTATCCCTGATCTGTGATTAACCGTATACCGCTTTGAGTGAAGTAT 5709
Db 6130 TTTCTCGGTTATCCCTGATCTGTGATTAACCGTATACCGCTTTGAGTGAAGTAT 6071
QY 5710 ACCGCTCGCGCAACCGCTTCTCCCGCGGTTGCGGCTTCAATTAATGCGAG 5822
Db 6070 ACCGCTCGCGCAACCGCTTCTCCCGCGGTTGCGGCTTCAATTAATGCGAG 5769
QY 5770 CGCCCAATAGCAACCGCTTCTCCCGCGGTTGCGGCTTCAATTAATGCGAG 6011
Db 6010 CGCCCAATAGCAACCGCTTCTCCCGCGGTTGCGGCTTCAATTAATGCGAG 5958

RESULT 12
US-08-675-566-25/c
; Sequence 25, Application US/08675566
; Patent No. 6090393
; GENERAL INFORMATION:
; APPLICANT: Fischer, Laurent
; TITLE OF INVENTION: PROMOTERS, EXPRESSION CASSETTES,
; TITLE OF INVENTION: RECOMBINANT VIRUSES, METHODS FOR MAKING, AND USES THEREOF
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,566
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer Esq., William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2890
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)840-3333
; TELEFAX: (212)840-0712
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8792 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-675-566-25

Query Match 43.9%; Score 2553; DB 3; Length 8792;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2632; Conservative 0; Mismatches 5; Indels 56; Gaps 2;

QY 3134 CCCAATTCGCCCTTAGTGAGTCGTATTACAACTTAATCGCTTGGAGCACATCCCGCTTGC 3193
Db 8773 CCCAATTCGCCCTTAGTGAGTCGTATTACAACTTAATCGCTTGGAGCACATCCCGCTTGC 8714
QY 3194 GACTGGGAAACCCCTGGGCTTACCCAACTTAATCGCTTGGAGCACATCCCGCTTGC 3253
Db 8713 GACTGGGAAACCCCTGGGCTTACCCAACTTAATCGCTTGGAGCACATCCCGCTTGC 8654
QY 3254 AGCTGGCTAATAGCGAGAGCGCCGACCGATCGCCCTTCCCAACAGTTGGCAGCGCTG 3313

Db 8653 AGCTGGCTAATAGCGAGAGCGCCGACCGATCGCCCTTCCCAACAGTTGGCAGCGCTG 8594
QY 3314 AATCGCGAATG---GACGCGCCCTGTAGCGCGCGCATTAAGCGCGCGGCTGTGTGTGTT 3369
Db 8593 AATCGCGAATGGCGGAGCGCCCTGTAGCGCGCGCATTAAGCGCGCGGCTGTGTGTGTT 8534
QY 3370 ACGGCGAGCGTACCGCTACACATTGCCAGCGCCCTAGCGCGCTTCCCTTTCGCTTTTC 3429
Db 8533 ACGGCGAGCGTACCGCTACACATTGCCAGCGCCCTAGCGCGCTTCCCTTTCGCTTTTC 8474
QY 3430 CTTTCCTTTCTCGCAGCTTTCGCGCGCTTCCCGCTCAAGCTCTAAATCGGGGCTCCCT 3489
Db 8473 CTTTCCTTTCTCGCAGCTTTCGCGCGCTTCCCGCTCAAGCTCTAAATCGGGGCTCCCT 8414
QY 3490 TTAGGGTTCGGAATTTAGAGCTTTACGGCACCTCGACCGCAAAACCTTGAATTCGGTGTAT 3549
Db 8413 TTAGGGTTCGGAATTTAGTCTTTAGCGCACCTCGACCGCAAAACCTTGAATTCGGTGTAT 8354
QY 3550 GGTTCAGTATGCGGCGCATCGCCCTGATAGACGGTTCCTTTCGCGCTTTGAGCTGGAGTCC 3609
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QY 3610 ACGTTCTTTAATAGTGGACTCTTGTCCAACTGGAAACACACTCAACCCCTATCTCGGTC 3669
Db 8293 ACGTTCTTTAATAGTGGACTCTTGTCCAACTGGAAACACACTCAACCCCTATCTCGGTC 8234
QY 3670 TATTCCTTTGATTTAAGGGATTTTGGCGATTTTCGCGCTTATTTGGTTTAAATAAGAGCTG 3729
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QY 3730 ATTTAACAATATTTAAGCGGAATTTTAAACAAATATTAACGTTTACAATTC--- 3789
Db 8173 ATTTAACAATATTTAAGCGGAATTTTAAACAAATATTAACGTTTACAATTC--- 8121
QY 3790 GCGGTATTTTCTCTTACGATCTGCGGTATTTACACCGCATCAGTGGCAGCTTTT 3849
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QY 3850 CGGGGAAATGTGCGGGAACCCCTATTGTTTATTTTCTAAATACATTCAAATATGAT 3909
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QY 3970 AGTATTTCAACATTTCCGCTGCGCCCTTATTCCTTTTTCGCGCATTTTTCCTTCTGTT 4029
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QY 4150 GAACTTTTCCAAATGATGAGCAGCTTTTAAAGTTCTGCTATGTCGCGCGGTATATTCCTG 4209
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QY	5470	ACGAGGAGGAGCTTCCAGGGGAAAAACGCTCGTATCTTTATAGTCTCTGCGGGTTTCGCCAC	5520
Db	6485	ACGAGGAGGAGCTTCCAGGGGAAAAACGCTCGTATCTTTATAGTCTCTGCGGGTTTCGCCAC	6426
QY	5530	CTCTGACTTGAGCGTGCATTTTGTGATGCTCTCAGGGGGGCGAGCCCTATGGA AAAAC	5589
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QY	5590	GCCAGCAACCGCGCTTTTACGGTTCCTTCGGCCTTTTGTCTGGCCTTTTGTCTGCTCATGTTTC	5649
Db	6365	GCCAGCAACCGCGCTTTTACGGTTCCTTCGGCCTTTTGTCTGGCCTTTTGTCTCATGTTTC	6306
QY	5650	TTTCTCGTTATCCCTCGATTCTGTGGATAACCGTATTAACGGCTTTGAGTGAGCTGAT	5709
Db	6305	TTTCTCGTTATCCCTCGATTCTGTGGATAACCGTATTAACGGCTTTGAGTGAGCTGAT	6246
QY	5710	ACCCTCGCGCAGCCGAAACGACCGAGCGCAGCGAGTCAGTGACGAGGAAAGCGGAAAG	5769
Db	6245	ACCCTCGCGCAGCCGAAACGACCGAGCGCAGCGAGTCAGTGACGAGGAAAGCGGAAAG	6186
QY	5770	CGCCCAATACGCAAAACCGCTCTCTCCCGCGCGTTTGGCGATTCAATTAATGCAG	5822
Db	6185	CGCCCAATACGCAAAACCGCTCTCTCCCGCGCGTTTGGCGATTCAATTAATGCAG	6133
RESULT 13			
US-09-608-730B-21			
; Sequence 21, Application US/09608730B			
; Patent No. 6423344			
; GENERAL INFORMATION:			
; APPLICANT: Hardy, Stephen			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PRODUCING RECOMBINANT			
; TITLE OF INVENTION: VIRIONS			
; FILE REFERENCE: PP01569.101			
; CURRENT APPLICATION NUMBER: US/09/608,730B			
; CURRENT FILING DATE: 2000-06-30			
; PRIOR APPLICATION NUMBER: 09/476,299			
; PRIOR FILING DATE: 1999-12-30			
; NUMBER OF SEQ ID NOS: 29			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 21			
; LENGTH: 4883			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Description of Artificial Sequence: pBS CP			
US-09-608-730B-21			
Query Match 43.8%; Score 2550; DB 4; Length 4883;			
Best Local Similarity 97.7%; Pred. No. 0;			
Matches 2629; Conservative 0; Mismatches 5; Indels 56; Gaps			
QY	3134	CCCAATTGCCCTATAGTCAGTCGATTACAACTTCACTGGCGCTCGTTTACAACTCGT	3139
Db	1984	CCCAATTGCCCTATAGTCAGTCGATTACAACTTCACTGGCGCTCGTTTACAACTCGT	204
QY	3194	GACTGGGAAAACCTTGGCGTTACCCAACTTAATCGCTTGCAGCACATCCCCCTTTGCGC	325
Db	2044	GACTGGGAAAACCTTGGCGTTACCCAACTTAATCGCTTGCAGCACATCCCCCTTTGCGC	210
QY	3254	AGCTGCGGTAATAGCAAGAGCCCGCAACCGATGCGCCTTCCCAACAGTTGGCAGCTG	331
Db	2104	AGCTGCGGTAATAGCAAGAGCCCGCAACCGATGCGCCTTCCCAACAGTTGGCAGCTG	216
QY	3314	AATGGCGAAT- GGAACGGCCCTGTAGCGGGCGAATTAAGCGCGCGGTGTGGTGTACG	337
Db	2164	AATGGCGAATGGGACGCGCCCTGTAGCGGGCGAATTAAGCGCGCGGTGTGGTGTACG	222
QY	3373	CGCAGCGTGACCGCTACACTTGCACGCGCCCTAGCGCCGCTCTTTTCGCTTTCCCT	343
Db	2224	CGCAGCGTGACCGCTACACTTGCACGCGCCCTAGCGCCGCTCTTTTCGCTTTCCCT	228
QY	3433	TCCTTTTTCGCCACGTTGCGCGCGCTTTCGCCGTCAGACTTAATCGGGGGCTCCCTT	349

QY	4390	GGACCGAAGAGACTAACCGCTTTTGTGCAACAATGGGGGATCATGTAACTCGCCTTGAT	4449
DB	7565	GGACCGAAGAGACTAACCGCTTTTGTGCAACAATGGGGGATCATGTAACTCGCCTTGAT	7506
QY	4450	CGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGAGCGGTGACACCAAGTGCCT	4509
DB	7505	CGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGAGCGGTGACACCAAGTGCCT	7446
QY	4510	GTAGCANTGCAACACGTTGCGCAAACTATTAACTGCGCAACTACTTACTCTAGCTTCC	4569
DB	7445	GTAGCAATGGCAACACGTTGCGCAAACTATTAACTGCGCAACTACTTACTCTAGCTTCC	7386
QY	4570	CGGCAACAAATTAATAGACTGGATGGAGCGGATAAAGTTGCAAGGACCACTTCGCGCTCG	4629
DB	7385	CGGCAACAAATTAATAGACTGGATGGAGCGGATAAAGTTGCAAGGACCACTTCGCGCTCG	7326
QY	4630	GCCCTTCGGCTGGCTGGTTTATGCTGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGC	4689
DB	7325	GCCCTTCGGCTGGCTGGTTTATGCTGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGC	7266
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QY	5050	CGCTACCAAGCCGTGTTGTTGTCGGATCAAGAGTACCAACTCTTTTTCGGAAGGTA	5109
DB	6905	CGCTACCAAGCCGTGTTGTTGTCGGATCAAGAGTACCAACTCTTTTTCGGAAGGTA	6846
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DB	6785	CACCACTTCAAGAACTCTGTAGCACCGGCTACATACCTCGCTCTGCTTAATCTCTTACCA	6726
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DB	6665	CGGATAAGGCGCAGCGGTGCGGCTGAACCGGGGGTTCTGTGCACACAGCCGAGTTGGAG	6606
QY	5350	CGAACGACTTACACCGAACTGAGATACCTTACAGCGTGAAGCTATGAGAAAGCCGAGCTT	5409
DB	6605	CGAACGACTTACACCGAACTGAGATACCTTACAGCGTGAAGCTATGAGAAAGCCGAGCTT	6546
QY	5410	CCCGAAGGGAAGAGCGGACAGGTATCCGTTAAGCGCAGGTCGGAAACAGGAGAGCGC	5469
DB	6545	CCCGAAGGGAAGAGCGGACAGGTATCCGTTAAGCGCAGGTCGGAAACAGGAGAGCGC	6486

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Qy GGGTTCCGATTTAGAGCTTTACGCGACCTCGACCGCAAAAACCTTGATTTGGGTGATGGT 3552
Db GGGTTCCGATTTAGTGGCTTTACGCGACCTCGACCGCAAAAACCTTGATTTAGGGTGTGGT 2403
Qy TCAGTGTAGTGGGCGCATCGCCCTGATAGACGGTTTTTCGCGCTTTGAGCTTGGAGTCCACG 3612
Db TCAGTGTAGTGGGCGCATCGCCCTGATAGACGGTTTTTCGCGCTTTGAGCTTGGAGTCCACG 2463
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Qy TGGGAACCGGAGCTGAATGAACCAATACCAACGACGAGCGTGAACACGATGCTGTA 4512
Db TGGGAACCGGAGCTGAATGAACCAATACCAACGACGAGCGTGAACACGATGCTGTA 3308
Qy GCAATGGCAACGCTTGGCGAAAATAATTAACCTGGCGAACTACTTACTTACTTCCCGG 4572
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Db 3309 GCAATGGCAACAGCTTTCGCGAAACTATTAACCTGGCGAACTACTTACTTACTTCCCGG 3368
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Qy 5473 AGGAGCTTCCAGGGGAAACCGCTGTATCTTTATAGTCTGTGCGGTTCGCGCACCTC 5532
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Qy 5533 TGACTTGAGCGTTCGATTTTGTGATGCTCGTCAGGGGCGGAGCTTATGAGAAACGCC 5592
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RESULT 14
US-08-659-206A-1
; Sequence 1, Application US/08659206A
; Patent No. 5922685
; GENERAL INFORMATION:
; APPLICANT: Rakhmievich, Alexander
; TITLE OF INVENTION: IL-12 Gene Therapy of Tumors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,206A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 110229.91144
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7287 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Plasmid DNA"
; IMMEDIATE SOURCE:
; CLONE: pWRG3169
; FEATURE:
; NAME/KEY: promoter
; LOCATION: 1..628
; NAME/KEY: iDNA
; LOCATION: 629..810
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(953..1258, 1332..1673)
; OTHER INFORMATION: /product= "p35 gene product"
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 1797..2024
; FEATURE:
; NAME/KEY: promoter
; LOCATION: 2110..2737
; FEATURE:
; NAME/KEY: iDNA

; LOCATION: 2738..2919
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2983..3990
; OTHER INFORMATION: /product= "p40 gene product"
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 4075..4306
; US-08-659-206A-1

Query Match 43.8%; Score 2550; DB 2; Length 7287;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2629; Conservative 0; Mismatches 5; Indels 56; Gaps 2;
QY 3134 CCCAATTGCGCCCTATAGTAGTCTGATTACAAATTCACCTGCGCGCTGTTTACAGCTCGT 3193
Db 4355 CCCAATTGCGCCCTATAGTAGTCTGATTACAAATTCACCTGCGCGCTGTTTACAGCTCGT 4414
QY 3194 GACTGGGAAACCCCTGGCGTTACCCAACTTAATGCCTTGCGACATCCGCCCTTTCGCC 3253
Db 4415 GACTGGGAAACCCCTGGCGTTACCCAACTTAATGCCTTGCGACATCCGCCCTTTCGCC 4474
QY 3254 AGCTGGCGTAATAGCGAAGAGCGCGCACCGATGCCCTTCCCAACAGTTGCGAGCCTG 3313
Db 4475 AGCTGGCGTAATAGCGAAGAGCGCGCACCGATGCCCTTCCCAACAGTTGCGAGCCTG 4534
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QY 3373 GCGAGCGTAGCGGTACACTTTCGCGAGCGCGCTAGCGCGCGCTTTCGCTTTCCTTCCCT 3432
Db 4595 GCGAGCGTAGCGGTACACTTTCGCGAGCGCGCTAGCGCGCGCTTTCGCTTTCCTTCCCT 4654
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Db 4715 GGGTTCGGAATTAGTGTCTTACGCGACCTCGACCGCAAAACCTTGATTTGGGTGATGCT 4774
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QY 3613 TTCTTTAATAGTGGACTCTTGTTCCAAACCTGGAACAACTCAACCTATCTCGGTCTAT 3672
Db 4835 TTCTTTAATAGTGGACTCTTGTTCCAAACCTGGAACAACTCAACCTATCTCGGTCTAT 4894
QY 3673 TCTTTTGATTTATAAGGGATTTTTCGCGATTTTCGCGCTATTTGGTTAAATAATGAGCTGAT 3732
Db 4895 TCTTTTGATTTATAAGGGATTTTTCGCGATTTTTCGCGCTATTTGGTTAAATAATGAGCTGAT 4954
QY 3733 TAACAAATATTAAACGGAATTTTAACAAAATTAACGTTTACAATTTTCGCGCTGATGCG 3792
Db 4955 TAACAAATATTAAACGGAATTTTAACAAAATTAACGTTTACAATTTTTCGCGCTGATGCG 5003
QY 3793 GTATTTCTCTTACGCATCTGTGCGGTATTTTACACCGCATACAGTGGCACTTTTCGG 3852
Db 5004 -----AGTGGCACTTTTCGG 5019
QY 3853 GGAATGTGCGGAAACCCCTATTTGTTTATTTTCTAAATACATTTCAATATGATATCCG 3912
Db 5020 GGAATGTGCGGAAACCCCTATTTGTTTATTTTCTAAATACATTTCAATATGATATCCG 5079
QY 3913 CTCTAGAGCAATAACCCCTGATAAATGCTTCAATAATATTGAAAAAGAGAGATGAGT 3972
Db 5080 CTCTAGAGCAATAACCCCTGATAAATGCTTCAATAATATTGAAAAAGAGAGATGAGT 5139
QY 3973 ATTCAACATTTCCGTTGTCGCCCTTATTCCTTTTTCGCGCAATTTTGGCTTCTCTGTTTT 4032
Db 5140 ATTCAACATTTCCGTTGTCGCCCTTATTCCTTTTTCGCGCAATTTTGGCTTCTCTGTTTT 5199

SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,809B
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,846
FILING DATE: March 9, 1994
APPLICATION NUMBER: 07/789,919
FILING DATE: No. 592564ember 6, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 214/212
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6345 bases
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-472-809B-7

Query Match 43.8%; Score 2549; DB 2; Length 6345;

Beat Local Similarity 97.7%; Pred. No. 0;
Matches 2628; Conservative 0; Mismatches 5; Indels 56; Gaps 2;

QY	3135	CAAAATCGCCCTATAGTGGTACCACTTAATCGGCTTGACGACATCCCTTTTCGCCA	3194
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QY	3195	ACTGGGAAACCCCTGGCGTTACCACTTAATCGGCTTGACGACATCCCTTTTCGCCA	3254
DB	2832	ACTGGGAAACCCCTGGCGTTACCACTTAATCGGCTTGACGACATCCCTTTTCGCCA	2773
QY	3255	GCTGGGTAATAGCGAAGGCGCGACGATCGCCCTTCCCAACAGTTGCGCGCTGA	3314
DB	2772	GCTGGGTAATAGCGAAGGCGCGACGATCGCCCTTCCCAACAGTTGCGCGCTGA	2713
QY	3315	ATGGCGAAT-GGACGGCCCTGTAGCGGCGCATTAAGCGCGCGGTGGTGGTATCGC	3373
DB	2712	ATGGCGAATGGACGGCCCTGTAGCGGCGCATTAAGCGCGCGGTGGTGGTATCGC	2653
QY	3374	GCAGCGTACCGCTACACTTGCAGCGCCCTAGCGCCCGCTCTTTTCCCTTT	3433
DB	2652	GCAGCGTACCGCTACACTTGCAGCGCCCTAGCGCCCGCTCTTTTCCCTTT	2593
QY	3434	CTTTTTCGCGAGTTTCGGGCTTTCGGGCTCAAGCTCAATTCGGGGCTCCCTTAG	3493
DB	2592	CTTTTTCGCGAGTTTCGGGCTTTCGGGCTCAAGCTCAATTCGGGGCTCCCTTAG	2533
QY	3494	GGTTCGATTTAGAGCTTTACGCGACCTCGACCGCAAAAACCTTGATTTGGGTGATGTT	3553
DB	2532	GGTTCGATTTAGAGCTTTACGCGACCTCGACCGCAAAAACCTTGATTTAGGTTGATGTT	2473
QY	3554	CACGTAAGTGGGCAATCGCCCTGATAGAGGTTTTTTCGGCTTTTGAAGTGGAGTCAAGT	3613
DB	2472	CACGTAAGTGGGCAATCGCCCTGATAGAGGTTTTTTCGGCTTTTGAAGTGGAGTCAAGT	2413
QY	3614	TCATTAATAGTGACCTTTGTTCCAACTGGAAACACACTCAACCTATCTCGGCTATT	3673
DB	2412	TCATTAATAGTGACCTTTGTTCCAACTGGAAACACACTCAACCTATCTCGGCTATT	2353
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DB	2352	CTTTTGATTTAAGGATTTTTCGGGCTATTTGGCTATTTGGTTAAAAAATGAGCTGATT	2293
QY	3734	AACAATATTTAAGCGAATTTTAAACAAATATTAAGTTTACATTTTCGCTGATCGCG	3793

DB	2292	AACAAAATTTAAGCGAATTTTAAACAAAATATTAAACGCTTCAATTT	2245
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QY	3854	GAATGTGCGCGGAACCCCTATTTTGTATTTTCTAAATACATTCAATATGTATCGC	3913
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QY	3914	TCATGAGACAAATACCCCTGATAATGCTTCAATAATTTGAAAAGGAAGAGTATGAGTA	3973
DB	2167	TCATGAGACAAATACCCCTGATAATGCTTCAATAATTTGAAAAGGAAGAGTATGAGTA	2108
QY	3974	TTCAACATTTCCGTTGTCGCCCTTATTCCTTTTTCGGGCAATTTTTCCTGTTTTCG	4033
DB	2107	TTCAACATTTCCGTTGTCGCCCTTATTCCTTTTTCGGGCAATTTTTCCTGTTTTCG	2048
QY	4034	CTACCCGAGAAACCGTGTGTAAGATGCTGAAGATCAGTTGGTGCACAGTGG	4093
DB	2047	CTACCCGAGAAACCGTGTGTAAGATGCTGAAGATCAGTTGGTGCACAGTGG	1988
QY	4094	GTACATCGAACTGGATCTCAACAGCGGTAAAGATCCTTTGAGAGTTTTCGCCCGGAAGAC	4153
DB	1987	GTACATCGAACTGGATCTCAACAGCGGTAAAGATCCTTTGAGAGTTTTCGCCCGGAAGAC	1928
QY	4154	GTTCCTCAATGATGAGCACTTTTAAAGTTCTGCTATGTCGGCGGTATTTATCCGCTATTG	4213
DB	1927	GTTCCTCAATGATGAGCACTTTTAAAGTTCTGCTATGTCGGCGGTATTTATCCGCTATTG	1868
QY	4214	ACGCGGCGAAGAGCACTCGGTGCGCGCATACACTATTCTCAGAAATGACCTGGTTGAGT	4273
DB	1867	ACGCGGCGAAGAGCACTCGGTGCGCGCATACACTATTCTCAGAAATGACCTGGTTGAGT	1808
QY	4274	ACTCACAGTACACAAAAGCATCTTACGGATGCGATGACAGTAAGAGAAATTTATCGAGTG	4333
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QY	4334	CTGCCATAACCATGATGATTAACACATGCGCGCCAACTTACTCTGACACAGTTCGGAGAC	4393
DB	1747	CTGCCATAACCATGATGATTAACACATGCGCGCCAACTTACTCTGACACAGTTCGGAGAC	1688
QY	4394	CGAAGAGTAAACCGCTTTTTCGACCAATGCGGGATCATGTAATCTGCTGCTGATCGTT	4453
DB	1687	CGAAGAGTAAACCGCTTTTTCGACCAATGCGGGATCATGTAATCTGCTGCTGATCGTT	1628
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QY	4514	CAATGGCAACACGTTGCGCAAACTATTAACTGGCGCACTTACTTACTAGCTTCCCGGC	4573
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DB	1507	ACAAATTAATGAGTGGATGGAGGGGATTAAGTTTCAGACCACTTCTGCGCTCGGCC	1448
QY	4634	TTCCGCTCGCTGTTTATTTGCTGATAAATCTGGAGCCGCTGAGCGGTCTCGCGGTA	4693
DB	1447	TTCCGCTCGCTGTTTATTTGCTGATAAATCTGGAGCCGCTGAGCGGTCTCGCGGTA	1388
QY	4694	TCATTCAGCACTGGGGCCAGATGGTAAAGCCCTCCGTATCTAGTATCTACACGCG	4753
DB	1387	TCATTCAGCACTGGGGCCAGATGGTAAAGCCCTCCGTATCTAGTATCTACACGCG	1328
QY	4754	GGAGTCAGCACTATGGATGAACGAAATAGACAGATCGCTGAGATAGTGGTCCCTCACTGA	4813
DB	1327	GGAGTCAGCACTATGGATGAACGAAATAGACAGATCGCTGAGATAGTGGTCCCTCACTGA	1268
QY	4814	TTAAGCATTTGGTAACTGTGACGCAAGTTTACTCATATATCTTTAGATTTGATTTAAAC	4873
DB	1267	TTAAGCATTTGGTAACTGTGACGCAAGTTTACTCATATATCTTTAGATTTGATTTAAAC	1208

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2004, 14:36:08 ; Search time 1542 Seconds
(without alignments)

17296.434 Million cell updates/sec

Title: US-09-924-197-1

Perfect score: 5822

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Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*
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19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2768	47.5	4773	10	US-09-991-209-32
3	2768	47.5	4950	10	US-09-991-209-34
4	2768	47.5	4965	10	US-09-991-209-37
5	2768	47.5	4974	10	US-09-991-209-35
6	2768	47.5	5001	10	US-09-991-209-40
7	2768	47.5	5034	10	US-09-991-209-33
8	2768	47.5	5164	10	US-09-991-209-36
9	2768	47.5	5277	10	US-09-991-209-25
10	2768	47.5	5295	10	US-09-991-209-38
11	2768	47.5	5327	10	US-09-991-209-27
12	2768	47.5	5337	10	US-09-991-209-19
13	2768	47.5	5337	10	US-09-991-209-23
14	2768	47.5	5337	10	US-09-991-209-31

15	2768	47.5	5338	10	US-09-991-209-15	Sequence 15, Appl
16	2768	47.5	5338	10	US-09-991-209-29	Sequence 29, Appl
17	2768	47.5	5345	10	US-09-991-209-17	Sequence 17, Appl
18	2768	47.5	5387	10	US-09-991-209-41	Sequence 41, Appl
19	2768	47.5	5395	10	US-09-991-209-21	Sequence 21, Appl
20	2683.4	46.1	3448	15	US-10-128-590-6	Sequence 6, Appl
21	2683.4	46.1	3448	15	US-10-128-587A-6	Sequence 6, Appl
22	2683.4	46.1	3448	16	US-10-128-578B-6	Sequence 6, Appl
23	2675.4	46.0	3018	13	US-09-486-142-7	Sequence 7, Appl
24	2670.2	45.9	3357	15	US-10-161-403-96	Sequence 96, Appl
25	2552	43.8	10078	14	US-10-033-190-3	Sequence 3, Appl
26	2549.4	43.8	2962	15	US-10-033-399B-10	Sequence 10, Appl
27	2549.4	43.8	3057	15	US-10-033-399B-23	Sequence 23, Appl
28	2549.4	43.8	3093	15	US-10-033-399B-7	Sequence 7, Appl
29	2549.4	43.8	5251	14	US-10-153-159-17	Sequence 17, Appl
30	2549.4	43.8	5251	15	US-10-153-176-17	Sequence 17, Appl
31	2549.4	43.8	5251	16	US-10-443-134A-17	Sequence 17, Appl
32	2549	43.8	2958	15	US-10-220-262-2	Sequence 2, Appl
33	2549	43.8	2958	15	US-10-220-262-3	Sequence 3, Appl
34	2549	43.8	2958	15	US-10-220-262-4	Sequence 4, Appl
35	2549	43.8	3351	16	US-10-014-099F-72	Sequence 72, Appl
36	2549	43.8	4754	16	US-10-014-099F-80	Sequence 80, Appl
37	2549	43.8	4773	16	US-10-014-099F-81	Sequence 81, Appl
38	2549	43.8	4831	16	US-10-014-099F-99	Sequence 99, Appl
39	2548.8	43.8	8858	15	US-10-378-393-1	Sequence 1, Appl
40	2538.2	43.6	10597	15	US-10-057-108-10	Sequence 10, Appl
41	2538.2	43.6	10599	15	US-10-057-108-11	Sequence 11, Appl
42	2538.2	43.6	12482	15	US-10-057-108-7	Sequence 7, Appl
43	2531.2	43.5	5175	15	US-10-057-108-6	Sequence 6, Appl
44	2531.2	43.5	8426	15	US-10-163-899-1	Sequence 1, Appl
45	2515	43.2	13910	10	US-09-919-901-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-924-197-1
; Sequence 1, Application US/09924197
; Publication No. US20030018993A1
; GENERAL INFORMATION:
; APPLICANT: Gutterson, Neal
; APPLICANT: Oeller, Paul
; TITLE OF INVENTION: Improved Methods of Gene Silencing Using Inverted
; TITLE OF INVENTION: Repeat Sequences
; FILE REFERENCE: 012176-010810US
; CURRENT APPLICATION NUMBER: US/09/924,197
; CURRENT FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 60/225,508
; PRIOR FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 5822
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-09-924-197-1

Query Match	100.0%	Score 5822;	DB 13;	Length 5822;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 5822;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CTGCGACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAG	60	
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Qy	61	TTAGTCACTCATTTAGGACCCCGAGCTTTACACTTTTATGCTTCGGCTCGTATGTTGTG	120	
Db	61	TTAGTCACTCATTTAGGACCCCGAGCTTTACACTTTTATGCTTCGGCTCGTATGTTGTG	120	
Qy	121	TGGAAATGTGAGCGGATAACAAATTTACACAGGAAACAGCTATGACCATGATTCAGCGCAA	180	
Db	121	TGGAAATGTGAGCGGATAACAAATTTACACAGGAAACAGCTATGACCATGATTCAGCGCAA	180	

QY	181	GCTATTAGGTGACCTATAGAATACTCAAGCTATGCATCCCAACGCGTTGGAGCTCTCC	240
DB	181		
QY	181	GCTATTTAGGTGACCTATAGAATACTCAAGCTATGCATCCCAACGCGTTGGAGCTCTCC	240
DB	241	CATATGTCGACCTGCAAGCGCGCGCACTAGTGAATGCTTAGATCTCGAGTGGAGCTAAT	300
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QY	301	TCTCAGTCCAAAGCCTCAACAAGTCAAGGTCAAGAGTCTCCTCAAGCAATCTAGTGGAGCTAAT	360
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QY	361	TACAGGAGATCAATGAAGAATCTTCAATCAAAAGTAAACTACTGTTCCAGCACATGCATCA	420
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QY	421	TGGTCAGTAAAGTTCAGAAAAGACATCCACCGGAAGACTTAAAGTTAGTGGGCATCTTTG	480
DB	421		
QY	481	AAAGTAACTTGTCAACATCCAGCAGCTGGCTGCTGGGGCCACAGACAAAAAGGAATGGT	540
DB	481		
QY	541	GCAGAAATGTTAGGCGCACCTACCAAAAGCACTTTGCTCTTATTCGAAAGATAAAGCAG	600
DB	541		
QY	601	ATTCTCTAGTACAAGTGGGAAACAAATTAAGTGGAAAGAGCTGCTTGACAGCCAC	660
DB	601		
QY	661	TCACCTAATGCGTATGACGAAACGAGTGCAGCCACCAAAAGAAATTAGCTTGAGCTCAGGAT	720
DB	661		
QY	721	TTAGCAGCATTTCCAGATGGGTTCAATCAACAAGTACGAGCCATATCACTTTTATTCAAA	780
DB	781	TTGGTATCGCCAAAACCAAGAGGAACCTCCATCCTCAAGGTTGTGAAGGAAGATTTCT	840
DB	781		
QY	841	CAGTCCAAAGCCTCAACAAGTCAAGGTCAAGGTCAAGTCTCCAAACCAATAGCCAAAAGCTAC	900
DB	841		
QY	901	AGGAGATCAATGAAGAATCTTCAATCAAAAGTAAACTACTGTTCCAGCACATGCATCATGG	960
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QY	961	TCAGTAAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCTTTGAAA	1020
DB	961		
QY	1021	GTAATCTGTCAACATCGAGCAGCTGGCTGTTGGGACACAGACAAAAAGGAATGGTGCA	1080
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QY	1081	GAATTTGTAGGCGCACCTACCAAAAGCATCTTTGCCCTTTATTGCAAGATAAAGCAGATT	1140
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QY	4621	CTGGCTCGGCGCTTCCGGCTGGCTGGTTTATTTCTGTGATAAATCTGGAGCGGTTAGCGT	4690
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QY	4921	CTCATGACCAATCCCTTAAAGTGGTTTCTTCCACTGAGCGTCAAGCCCGGTAGAA	4980
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Db	5101	CGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAATACCTCTCTAGTAGCGG	5160
QY	5161	TAGTTAGGCGCACCTTCAAGAACTCTGTAGCACCGCCTACATACCTGCTCTGTAATC	5220
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QY	5221	CTGTACAGTGGCTGCTGCGAGTGGCGATAGTGTGCTTACCGGGTGGACTCAAGA	5280
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QY	5281	CGATAGTTACCGGATAGCGCAGCGGTGCGGCTGAACCGGGGGTTTCTGTCACACAGCC	5340
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QY	5401	GCACCGCTTCCGAAAGGAGAAAGCGGACAGGTATCCGTTAGCGGAGGTCGGAACA	5460
Db	5401	GCACCGCTTCCGAAAGGAGAAAGCGGACAGGTATCCGTTAGCGGAGGTCGGAACA	5460
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Db	5461	GGAGAGCGCACGAGGAGCTTCCAGGGGGAAACCGCTGATCTTTATAGTCTCTGCGGG	5520
QY	5521	TTTGGCCACCTCTGACTGAGCGTGAATTTTGTGATGCTGCTGAGGGGGCGGAGCCTA	5580
Db	5521	TTTGGCCACCTCTGACTGAGCGTGAATTTTGTGATGCTGCTGAGGGGGCGGAGCCTA	5580
QY	5581	TGGAHAACGCGCACGAGCGCTTTTACGTTCTGCGCTTTTCTGCGCTTTTGTCT	5640
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; Sequence 32, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Morse, Phillip
; APPLICANT: Langdon, Timothy
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 4773
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pGt6 vector
US-09-991-209-32

Query Match 47.5%; Score 2768; DB 10; Length 4773;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2895; Conservative 0; Mismatches 25; Indels 72; Gaps 4;

QY	2835	AAGCAGATCGTTCAACATTTGGCAATAAAGTTCTTAAGATTGAATCCTGTTCCGGTC	2894
Db	778	AAGCAGATCGTTCAACATTTGGCAATAAAGTTCTTAAGATTGAATCCTGTTCCGGTC	837
QY	2895	TTGCGATGATTATCATATAATTTCTGTTGAAATTAAGTAAAGCATGTAATAATTAACATGT	2954
Db	838	TTGCGATGATTATCATATAATTTCTGTTGAAATTAAGTAAAGCATGTAATAATTAACATGT	897
QY	2955	AATGATGAGTTTATGATGAGTGGTTTATGATGAGTCCCGCAATTAATTAACATTT	3014
Db	898	AATGATGAGTTTATGATGAGTGGTTTATGATGAGTCCCGCAATTAATTAACATTT	957
QY	3015	ATACCGGATAGAAAACAAATATAGCGCAAACTAGGATAAATATCGCGCGGTGT	3074
Db	958	ATACCGGATAGAAAACAAATATAGCGCAAACTAGGATAAATATCGCGCGGTGT	1017
QY	3075	CATCTATGTTACTAGATCGACCTGAGGATGGATCCGCGCGCGATGCGACGTCCGGC	3134
Db	1018	CATCTATGTTACTAGATCGATAAGCTTCTAGAGCGCGCGGTGGAGC-----T 1064	
QY	3135	CCAAATTCGCCCTATAGTGTGCTATTAC---AATTCACCTGGCGTCTGTTTACACGTC	3191
Db	1065	CCAAATTCGCCCTATAGTGTGCTATTACCGCGCTCACTGGCGCTGTTTACACGTC	1124
QY	3192	GTCACTGGGAAACCCCTGGCGTTACCCAACTTAATCGCTTGACGACATCCCGCTTCG	3251

Db 1125 GTGACTGGGAAACCCCTGGCGTTTACCACTTAATCGCTTGCAGCACATCCCCCTTTG 1184
QY 3252 CCAGCTGGCTTAATAGCGAGAGCCCGCAGCCGATCGCCCTTCCCAACAGTTGGCAGCC 3311
Db 1185 CCAGCTGGCTTAATAGCGAGAGCCCGCAGCCGATCGCCCTTCCCAACAGTTGGCAGCC 1244
QY 3312 TGAATGGCGAAT -GGACGCGCCCTGTAGCGCGCATTAAGCGCGCGCGGTGTGGTGTGA 3370
Db 1245 TGAATGGCGAATGGAGCGCGCCCTGTAGCGCGCATTAAGCGCGCGCGGTGTGGTGTGA 1304
QY 3371 CGCGCAGCGTACCGCTACACTTGCAGCGCCCTAGCGCGCCCTTTCGCTTTCTTC 3430
Db 1305 CGCGCAGCGTACCGCTACACTTGCAGCGCCCTAGCGCGCCCTTTCGCTTTCTTC 1364
QY 3431 CTTCCCTTTCTCGCACGTTTCGCGGCTTTCGCGCTCAAGCTCAAAATCGGGGCTCCCTT 3490
Db 1365 CTTCCCTTTCTCGCACGTTTCGCGGCTTTCGCGCTCAAGCTCTAAATCGGGGCTCCCTT 1424
QY 3491 TAGGGTTCGGAATTAAGCTTTACGGCACCTCGACCGCAAAACCTTGATTTGGGTGATG 3550
Db 1425 TAGGGTTCGGAATTAAGCTTTACGGCACCTCGACCGCAAAACCTTGATTTGGGTGATG 1484
QY 3551 GTTCAGTAGTGGCCCATCGCCCTGTAGACGCTTTTCGCCCTTTGACGTTGGAGTCCA 3610
Db 1485 GTTCAGTAGTGGCCCATCGCCCTGTAGACGCTTTTCGCCCTTTGACGTTGGAGTCCA 1544
QY 3611 CGTCTTTTAATAGTGACCTTGTTCGAACTGGAACACACTCAACCCCTATCTCGGTCT 3670
Db 1545 CGTCTTTTAATAGTGACCTTGTTCGAACTGGAACACACTCAACCCCTATCTCGGTCT 1604
QY 3671 ATTCTTTGATTTAAGGATTTTCGCGCTATTCGCGCTATTCGTTTAAATAATGACTGA 3730
Db 1605 ATTCTTTGATTTAAGGATTTTCGCGCTATTCGCGCTATTCGTTTAAATAATGACTGA 1664
QY 3731 TTATAAATAATTAACCGGAATTTTAAACAAATATAACGTTTAAATTCGCGCTGATG 3790
Db 1665 TTATAAATAATTAACCGGAATTTTAAACAAATATAACGTTTAAATTCGCGCTGATG 1715
QY 3791 CGGTATTTCTCTTACGCTATCTGCGGTATTTACACCGCATACAGTGGCACTTTTC 3850
Db 1716 -----AGGTGGCACTTTTC 1729
QY 3851 GGGGAATGTGCGGGAACCCCTATTGTTTATTTTCTAAATAACATCAAAATATGATC 3910
Db 1730 GGGGAATGTGCGGGAACCCCTATTGTTTATTTTCTAAATAACATCAAAATATGATC 1789
QY 3911 CGCTCATGAGCAATAACCTGTAAATGCTTCAATAATATTGAAAGAAAGAGATGA 3970
Db 1790 CGCTCATGAGCAATAACCTGTAAATGCTTCAATAATATTGAAAGAAAGAGATGA 1849
QY 3971 GTATTCAACATTTCCGTGCGCCCTATTTCCTTTTTCGCGCAATTTGCGCTTCTGTTT 4030
Db 1850 GTATTCAACATTTCCGTGCGCCCTATTTCCTTTTTCGCGCAATTTGCGCTTCTGTTT 1909
QY 4031 TTGCTCACCCGAAACGCTGTGAAAGTAAAGATGCTGAAGATCAGTTGGGTGACGAG 4090
Db 1910 TTGCTCACCCGAAACGCTGTGAAAGTAAAGATGCTGAAGATCAGTTGGGTGACGAG 1969
QY 4091 TGGGTATCATCGAATGATCTCAACAGCGGTAGATCCTTGAGAGTTTTCGCCCGGAAG 4150
Db 1970 TGGGTATCATCGAATGATCTCAACAGCGGTAGATCCTTGAGAGTTTTCGCCCGGAAG 2029
QY 4151 AACGTTTTCGAATGATGACCTTTTAAAGTTTCTGCTATGTCGCGGTATTTCCCGTA 4210
Db 2030 AACGTTTTCGAATGATGACCTTTTAAAGTTTCTGCTATGTCGCGGTATTTCCCGTA 2089
QY 4211 TTGACGCGGCAAGAGCAACTCGGTGCGCGCATACACTATCTCAGAACTGCTTGGT 4270
Db 2090 TTGACGCGGCAAGAGCAACTCGGTGCGCGCATACACTATCTCAGAACTGCTTGGT 2149
QY 4271 AGTACTCACAGTACAGAAAGCATCTTACGATGGCATGACAGTAAGAGAAATTATGCA 4330
Db 2150 AGTACTCACAGTACAGAAAGCATCTTACGATGGCATGACAGTAAGAGAAATTATGCA 2209

QY 4331 GTGCTGCCATAACCATGAGTGATAACAACCTGGGCCAACTTACTTCTGCAACGATCGAG 4390
Db 2210 GTGCTGCCATAACCATGAGTGATAACAACCTGGGCCAACTTACTTCTGCAACGATCGAG 2269
QY 4391 GACCGAGGAGCTTAACCGCTTTTGTGCAACAATGGGGGATCATGTAACTCGCTTGCATC 4450
Db 2270 GACCGAGGAGCTTAACCGCTTTTGTGCAACAATGGGGGATCATGTAACTCGCTTGCATC 2329
QY 4451 GTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGAGCGTGACACCAAGTGCCTG 4510
Db 2330 GTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGAGCGTGACACCAAGTGCCTG 2389
QY 4511 TAGCAATGGCAACAAAGTTCGCAAACTATTAATCTGCGAACTACTTACTCTAGCTTCCC 4570
Db 2390 TAGCAATGGCAACAAAGTTCGCGCAAACTATTAATCTGCGAACTACTTACTCTAGCTTCCC 2449
QY 4571 GGCACCAATTAATAGACTGGAGCGGATAAAGTTGAGGACCACTTCTCGCTCGG 4630
Db 2450 GGCACCAATTAATAGACTGGAGCGGATAAAGTTGAGGACCACTTCTCGCTCGG 2509
QY 4631 CCCTTCCGCTGGCTGCTTATTGCTGATAAATCTGAGCCGCTGAGCGTGGCTCGCG 4690
Db 2510 CCCTTCCGCTGGCTGCTTATTGCTGATAAATCTGAGCCGCTGAGCGTGGCTCGCG 2569
QY 4691 GTATCATTTGAGCACTGGGCGCAGATGTAAGCCCTCCGCTATCTGATGTTATCTACACGA 4750
Db 2570 GTATCATTTGAGCACTGGGCGCAGATGTAAGCCCTCCGCTATCTGATGTTATCTACACGA 2629
QY 4751 CGGGGAGTCAGCACTATGATGAAGAAATAGACAGATCGCTGAGATGAGTGCCTCAC 4810
Db 2630 CGGGGAGTCAGCACTATGATGAAGAAATAGACAGATCGCTGAGATGAGTGCCTCAC 2689
QY 4811 TGATTAAGCAATTTGTAACCTGTCAGACCAAGTTTACTCATATATCTTTAGATGATTTAA 4870
Db 2690 TGATTAAGCAATTTGTAACCTGTCAGACCAAGTTTACTCATATATCTTTAGATGATTTAA 2749
QY 4871 AACTTCAATTTTAAATTTAAAGGATCTAGGTGAAGATCTTTTGTGATAATCTCATGACCA 4930
Db 2750 AACTTCAATTTTAAATTTAAAGGATCTAGGTGAAGATCTTTTGTGATAATCTCATGACCA 2809
QY 4931 AAATCCCTTAAGCTGAGTTTTCGTTCCACTGAGCGTCAGACCCCTAGAAAAAGATCAAG 4990
Db 2810 AAATCCCTTAAGCTGAGTTTTCGTTCCACTGAGCGTCAGACCCCTAGAAAAAGATCAAG 2869
QY 4991 GATCTTCTTGAGATCCTTTTTCGCGCTAATCTGCTGCTTGCACCAAAAAACAC 5050
Db 2870 GATCTTCTTGAGATCCTTTTTCGCGCTAATCTGCTGCTTGCACCAAAAAACAC 2929
QY 5051 CGCTACAGCGGTGTTTGTTCGCGATCAAGAGCTACCAACTCTTTTTCGAAAGTAA 5110
Db 2930 CGCTACAGCGGTGTTTGTTCGCGATCAAGAGCTACCAACTCTTTTTCGAAAGTAA 2989
QY 5111 CTGGCTTCAGAGCGCGATACAAATCTGCTTCTTCTAGTGTAGCGGTAGTGGCC 5170
Db 2990 CTGGCTTCAGAGCGCGATACCAATCTGCTTCTTCTAGTGTAGCGGTAGTGGCC 3049
QY 5171 ACCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTGCTAATCTGTTACAG 5230
Db 3050 ACCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTGCTAATCTGTTACAG 3109
QY 5231 TGGCTGTCGAGTGGCGATAAGTCTGTCTTACCGGTTTGGATCTCAAGAGATAGTTAC 5290
Db 3110 TGGCTGTCGAGTGGCGATAAGTCTGTCTTACCGGTTTGGATCTCAAGAGATAGTTAC 3169
QY 5291 CGGATAAGGCGCAGCGGTGGAACGGGGGTTTCGTGCACACAGCCCGCTTGGAGC 5350
Db 3170 CGGATAAGGCGCAGCGGTGGAACGGGGGTTTCGTGCACACAGCCCGCTTGGAGC 3229
QY 5351 GAACGACTACACCGAACTGAGATACCTACAGCGTGTGCTATGAGAAAGCGCAGCTTC 5410
Db 3230 GAACGACTACACCGAACTGAGATACCTACAGCGTGTGCTATGAGAAAGCGCAGCTTC 3289

Qy	4151	AACGTTTTCCAAATGATGAGCACTTTTAAAGTTCCTGCTATGTGGCGCGGTATTATCCCGTA	4210
Db	2207	AACGTTTTCCAAATGATGAGCACTTTTAAAGTTCCTGCTATGTGGCGCGGTATTATCCCGTA	2266
Qy	4211	TTGACGCGCGGCAAGAGCAACTCGGTCCGCGCATACACTATTCTCAGAATGACTTGGTTG	4270
Db	2267	TTGACGCGCGGCAAGAGCAACTCGGTCCGCGCATACACTATTCTCAGAATGACTTGGTTG	2326
Qy	4271	AGTACTCACCAAGTACACAAAAGACATCTTACGATGGCATGACAGTAAGAGAAATATGCA	4330
Db	2327	AGTACTCACCAAGTACACAAAAGACATCTTACGATGGCATGACAGTAAGAGAAATATGCA	2386
Qy	4331	GTGCTGCCATAACCATGAGTCATAAACACTGGGCGCAACTTACTTCTCACAACGATCGGAG	4390
Db	2387	GTGCTGCCATAACCATGAGTCATAAACACTGGGCGCAACTTACTTCTCACAACGATCGGAG	2446
Qy	4391	GACCGAAGGAGCTAACCGCTTTTTTGGACAACAATGGGGGATCATGTAACTCGCCTTGATC	4450
Db	2447	GACCGAAGGAGCTAACCGCTTTTTTGGACAACAATGGGGGATCATGTAACTCGCCTTGATC	2506
Qy	4451	GTTCGGAAACCGGAGCTGAATGAAGCCATACCAACGACGAGCGTGAACACACGATGCGTG	4510
Db	2507	GTTCGGAAACCGGAGCTGAATGAAGCCATACCAACGACGAGCGTGAACACACGATGCGTG	2566
Qy	4511	TAGCAATGGCAACAAACGTTGCGCAAACTATTAACTGGCGAACTTACTTCTAGCTTCCC	4570
Db	2567	TAGCAATGGCAACAAACGTTGCGCAAACTATTAACTGGCGAACTTACTTCTAGCTTCCC	2626
Qy	4571	GGCAACAATTAATAGACTGGATGGAGCGGATAAAGTTGCAGGACCACTTCTGCGTTCGG	4630
Db	2627	GGCAACAATTAATAGACTGGATGGAGCGGATAAAGTTGCAGGACCACTTCTGCGTTCGG	2686
Qy	4631	CCCTTCGGCTGGCTGGTTTATTCCTGATAAATCTGGAGCGGTGAGCGTGGTTCGGG	4690
Db	2687	CCCTTCGGCTGGCTGGTTTATTCCTGATAAATCTGGAGCGGTGAGCGTGGTTCGGG	2746
Qy	4691	GTATCATTTGCAGCACTGGGCGCAGATCGTAAAGCCCTCCCGTATCTGATGTTATCTACACGA	4750
Db	2747	GTATCATTTGCAGCACTGGGCGCAGATCGTAAAGCCCTCCCGTATCTGATGTTATCTACACGA	2806
Qy	4751	CGGGAGTCAGGCAACTATCGATGAACGAAATAGACAGATCGCTGAGATAGGTGCCTCAC	4810
Db	2807	CGGGAGTCAGGCAACTATCGATGAACGAAATAGACAGATCGCTGAGATAGGTGCCTCAC	2866
Qy	4811	TGATTAAGCATTCGTAACTCTCAGACCAAGTTTACTCATATATACTTTAGATTGATTTAA	4870
Db	2867	TGATTAAGCATTCGTAACTCTCAGACCAAGTTTACTCATATATACTTTAGATTGATTTAA	2926
Qy	4871	AACTTCATTTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTTTTTGATTAATCTCATGACCA	4930
Db	2927	AACTTCATTTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTTTTTGATTAATCTCATGACCA	2986
Qy	4931	AAATCCCTTAAAGTGAAGTTTCGTTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAAG	4990
Db	2987	AAATCCCTTAAAGTGAAGTTTCGTTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAAG	3046
Qy	4991	GATCTCTTCAGATCCCTTTTTTCTGGCGTAACTCTGCTGTGCAACAAAAAACCCAC	5050
Db	3047	GATCTCTTCAGATCCCTTTTTTCTGGCGTAACTCTGCTGTGCAACAAAAAACCCAC	3106
Qy	5051	CGCTACAGCGGTGGTTTGTTCGCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTTAA	5110
Db	3107	CGCTACAGCGGTGGTTTGTTCGCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTTAA	3166
Qy	5111	CTGCTTTCAGAGCGCAGATACCAAAATCTGCTCTTCTAGTGTAGCGGTAGTTAGGCC	5170
Db	3167	CTGCTTTCAGAGCGCAGATACCAAAATCTGCTCTTCTAGTGTAGCGGTAGTTAGGCC	3226
Qy	5171	ACCACATTCAAGAACTCTGTAGACCGGCTACATACCTCGCTCTGCTAAATCTGTGTACGAG	5230
Db	3227	ACCACATTCAAGAACTCTGTAGACCGGCTACATACCTCGCTCTGCTAAATCTGTGTACGAG	3286

QY	5231	TGGCTGCTCCAGTCGGCGATAAGTTCGTGTCCTTACCGGGTTGGACTCAAGACGATAGTTAC	5239
DB	3287	TGGCTGCTGCTCCAGTCGGCGATAAGTTCGTGTCCTTACCGGGTTGGACTCAAGACGATAGTTAC	3346
QY	5291	CGGATAGGGCGACGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCAGCTTCGAGC	5350
DB	3347	CGGATAGGGCGACGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCAGCTTCGAGC	3406
QY	5351	GAACGACCTACACGAACTGAGATACCTACAGCGTGTGAGCTATGAGAAAGCGCCACGCTTC	5410
DB	3407	GAACGACCTACACGAACTGAGATACCTACAGCGTGTGAGCTATGAGAAAGCGCCACGCTTC	3466
QY	5411	CCGAAGGAGGAAAGCGCGACAGGTATCCGTTAAGCGCAGGGTCGGAACAGGAGAGCGCA	5470
DB	3467	CCGAAGGAGGAAAGCGCGACAGGTATCCGTTAAGCGCAGGGTCGGAACAGGAGAGCGCA	3526
QY	5471	CGAGGAGCTTCCAGAGGGGAAAACCGCTGGGTATCTTTATGTCCTGTCGGGTTTCGCCACC	5530
DB	3527	CGAGGAGCTTCCAGAGGGGAAAACCGCTGGGTATCTTTATGTCCTGTCGGGTTTCGCCACC	3586
QY	5531	TCTGACTTGAGCGTCGATTTTGTGTGATGTCGTCAGGGGGCGGAGCCTATGAAAAACG	5590
DB	3587	TCTGACTTGAGCGTCGATTTTGTGTGATGTCGTCAGGGGGCGGAGCCTATGAAAAACG	3646
QY	5591	CCAGCAACGGGCCCTTTTACGGTTCCTGCGCTTTTGTGCGCTTTTGTGCTCACATGTTCT	5650
DB	3647	CCAGCAACGGGCCCTTTTACGGTTCCTGCGCTTTTGTGCGCTTTTGTGCTCACATGTTCT	3706
QY	5651	TTCTCTGAGTTATCCCTGATTTCTGTGGATAACGGTATTACCGCTTTTGTGAGTGCATGATA	5710
DB	3707	TTCTCTGAGTTATCCCTGATTTCTGTGGATAACGGTATTACCGCTTTTGTGAGTGCATGATA	3766
QY	5711	CCGCTCCGCCAGCGAAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAC	5770
DB	3767	CCGCTCCGCCAGCGGAAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAC	3826
QY	5771	GCCCAATACGCAAAACCGCTCTCCCGCGGGTTGGCCGATTCATTAATCGAG	5822
DB	3827	GCCCAATACGCAAAACCGCTCTCCCGCGGGTTGGCCGATTCATTAATCGAG	3878

RESULT 4

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RESOL. 4
US-09-991-209-37
; Sequence 37, Application US/09991209
; Publication No. US2003024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 4965
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pJQ3 vector
US-09-991-209-37

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Query Match      47.5%; Score 2768; DB 10; Length 4965;
Best Local Similarity 96.8; Pred. No. 0;
Matches 2895; Conservative 0; Mismatches 25; Indels 72; Gaps 4
QY      2835  AAGCAGATCGTTCAACAATTGGCAATAAAGTTTCTTTAAGATTCAATCCTCTTCCGCTC 2899
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1824 AACGAGATCGTTCACAACTTGGCAATAAAGTTTCTTAAGATTGAATCTCTGTGCGCGTC 1883 Db
2895 TTGGGATGATATCAATATATTTCTGTGTAATTAACGTTAAGCATGTAAATTAACATGT 2954 Qy
1884 TTGGGATGATATCAATATATTTCTGTGTAATTAACGTTAAGCATGTAAATTAACATGT 1943 Db
2955 AATGCATGAGCTTATTTATGAGATGGGTTTTATGATTAGAGTCCCGCAATTAACATTT 3014 Qy
1944 AATGCATGAGCTTATTTATGAGATGGGTTTTATGATTAGAGTCCCGCAATTAACATTT 2003 Db
3015 AATACGGATAGAAAAAATAATAGCGCGCAAACTAGGATAAATTAATCGCGCGGTGT 3074 Qy
2004 AATACGGATAGAAAAAATAATAGCGCGCAAACTAGGATAAATTAATCGCGCGGTGT 2063 Db
3075 CATCTATGTTACTAGATCGACTCGAGCATGGGATCGCGCGCGCATGCGACGTCGGGC 3134 Qy
2064 CATCTATGTTACTAGATCGAATGCTTCTAGAGCGCGCGGTGGAGC-----T 2110 Db
3135 CCAATTCGCCCTATAGTGAGTGGTATTAC---AATTCACTGGCGGTGGTTTTTACAAGTTC 3191 Qy
2111 CCAATTCGCCCTATAGTGAGTGGTATTACGGCGGTCACTGGCGGTGGTTTTTACAAGTTC 2170 Db
3192 GTGATCGGAAAAACCTTGGCGTTACCCAACTTAATCGCTTTGAGAGCATCCCGCTTTTCG 3251 Qy
2171 GTGATCGGAAAAACCTTGGCGTTACCCAACTTAATCGCTTTGAGAGCATCCCGCTTTTCG 2230 Db
3252 CCAGCTGGCGTAATAGCAAGAGCGCGCACCGATCGCCCTTCCCAACAGTTGCGAGCC 3311 Qy
2231 CCAGCTGGCGTAATAGCAAGAGCGCGCACCGATCGCCCTTCCCAACAGTTGCGAGCC 2290 Db
3312 TGAATGGCGAAT- GGACGCGGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGGTGTGA 3370 Qy
2291 TGAATGGCGAATGGACGCGGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGGTGTGA 2350 Db
3371 CGCGAGCGTGAACGCTACACTTGGCCAGGCGCTAGCGCGCGCTCTCTTTCGTTTCTTCC 3430 Qy
2351 CGCGAGCGTGAACGCTACACTTGGCCAGGCGCTAGCGCGCGCTCTCTTTCGTTTCTTCC 2410 Db
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2411 CTTCTCTTTCGCGACGTTTCCCGCTTCCCGTCAAGCTCTAATCGGGGCTCCCTT 2470 Db
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3611 CGTTCTTTAATAGTCGACTCTTGTTCCAAACCTGGAACAACACTCAACCTATCTCGGTCT 3670 Qy
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2711 TTTTAAACAATATTTTAAACGGAAATTTTAAACAATATTAACGTTTAAATTCGCGCTGATG 2761 Db
3791 CGGTATTTTCTCTTACGATCTGTGCGGTATTTTACACCGCATACAGGTGGCACTTTTC 3850 Qy
2762 -----AGGTGGCACTTTTC 2775 Db
3851 GGGGAAATGTGCGGAAACCCCTATTTGTTTATTTTCTTAAATATTAATTAATATGATATC 3910 Qy
2776 GGGGAAATGTGCGGAAACCCCTATTTGTTTATTTTCTTAAATATTAATTAATATGATATC 2835 Db
3911 CGCTCATGAGCAATTAACCTGATTAATGCTTCAATATTAATTTGAAAGGAAGAGATGGA 3970 Qy
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4031 TTGCTTCAACAGAAACGCTGTGAAAGTAAAGATGCTGAAGATCAGTTGGGTGCAACGAG 4090 Qy
2956 TTGCTTCAACAGAAACGCTGTGAAAGTAAAGATGCTGAAGATCAGTTGGGTGCAACGAG 3015 Db
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4151 AACGTTTTTCAATGATGAGCACTTTTAAAGTTTCTGCTATGTGGCGCGGTATTTATCCCGTA 4210 Qy
3076 AACGTTTTTCAATGATGAGCACTTTTAAAGTTTCTGCTATGTGGCGCGGTATTTATCCCGTA 3135 Db
4211 TTGACGCGCGGCAAGAGCACTCGGTGCGCGCATACACTATTTCTCAGAATGACTTGGTTG 4270 Qy
3136 TTGACGCGCGGCAAGAGCACTCGGTGCGCGCATACACTATTTCTCAGAATGACTTGGTTG 3195 Db
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3196 AGTACTCACAGTCAACAGAAAGCATCTTACGGATGGCATGACAGTAAAGAAATTTATGCA 3255 Db
4331 GTGCTGCCATTAACCATGAGTGATTAACACTGCGGCAACTTCTCTGACAGATCGGAG 4390 Qy
3256 GTGCTGCCATTAACCATGAGTGATTAACACTGCGGCAACTTCTCTGACAGATCGGAG 3315 Db
4391 GACCGAAGGAGCTAACCGCTTTTGGCACACATGGGGGATCATGTAACTCGCCCTTGATC 4450 Qy
3316 GACCGAAGGAGCTAACCGCTTTTGGCACACATGGGGGATCATGTAACTCGCCCTTGATC 3375 Db
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3376 GTTGGGAAACCGGAGCTGAATGAAGCCATACCAACAGCAGCGCTGACACCAAGATGCTG 3435 Db
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4571 GGCACAAATTAATAGCTGGAATGGAGCGGATAAAGTTGAGGACCACTTCTGCGCTCGG 4630 Qy
3496 GGCACAAATTAATAGCTGGAATGGAGCGGATAAAGTTGAGGACCACTTCTGCGCTCGG 3555 Db
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3556 CCTTCCGCTGGCTGGTTTATTTGCTGATAAATCTGGAGCCGCTGAGCGTGGGTCTCGCG 3615 Db
4691 GTATCATTTGACGACTGGGCGCAGATGTAAGCCCTCGCTATCTGATTTACTTACTACAGA 4750 Qy
3616 GTATCATTTGACGACTGGGCGCAGATGTAAGCCCTCGCTATCTGATTTACTTACTACAGA 3675 Db
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4811 TGATTAAGCAATTTGTTAACTGTGACAGCAAGTTTACTCATATATATCTTTAGATTTAA 4870 Qy
3736 TGATTAAGCAATTTGTTAACTGTGACAGCAAGTTTACTCATATATATCTTTAGATTTAA 3795 Db
4871 AACTTCATTTTAAATTTAAAGGATCTAGTGAAGATCGTTTTTGTATCTCATGACCA 4930 Qy
3796 AACTTCATTTTAAATTTAAAGGATCTAGTGAAGATCGTTTTTGTATCTCATGACCA 3855 Db
4931 AAATCCCTTAACTGAGTTTTTCCCTCACTGAGCGCTCAGACCCCGTAGAAGATCAAG 4990 Qy
3856 AAATCCCTTAACTGAGTTTTTCCCTCACTGAGCGCTCAGACCCCGTAGAAGATCAAG 3915 Db
4991 GATCTTCTTGAGATCCTTTTTTCTGCGCGTAATCTGTGCTGTGCAACAAAAAAAACAC 5050 Qy
3916 GATCTTCTTGAGATCCTTTTTTCTGCGCGTAATCTGTGCTGTGCAACAAAAAAAACAC 3975 Db

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QY 5051 CGCTACAGCGGTGGTTTGTTCGGGATCAAGAGCTACCAACTCTTTTCCGAAGTAA 5110
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QY 3976 CGCTACAGCGGTGGTTTGTTCGGGATCAAGAGCTACCAACTCTTTTCCGAAGTAA 4035
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QY 5111 CTGGCTTACAGAGCGCAGATACCAAAATAGTCTCTTCTAGTGTAGCGTAGTTAGGCC 5170
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QY 4036 CTGGCTTACAGAGCGCAGATACCAAAATAGTCTCTTCTAGTGTAGCGTAGTTAGGCC 4095
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QY 5171 ACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCTGCTAATCTGTTACCAG 5230
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QY 4096 ACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCTGCTAATCTGTTACCAG 4155
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QY 5231 TGCTGTCTCAGTGGCGATPAAGTCTGTCTTACCGGGTTGGACTCAAGACGATAGTTAC 5290
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QY 4156 TGCTGTCTCAGTGGCGATPAAGTCTGTCTTACCGGGTTGGACTCAAGACGATAGTTAC 4215
Db |||
QY 5291 CGGTAAGCGGCGAGCGTGGGCTGAACGGGGGTTCTGTGCAACAGCCGAGCTTGGAGC 5350
Db |||
QY 4216 CGGTAAGCGGCGAGCGTGGGCTGAACGGGGGTTCTGTGCAACAGCCGAGCTTGGAGC 4275
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QY 5351 GAACGACCTACACCGAACTGAGATACCTACAGCGTGAAGTTCGGAAACAGAGAGCGCA 5410
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QY 4276 GAACGACCTACACCGAACTGAGATACCTACAGCGTGAAGTTCGGAAACAGAGAGCGCA 4335
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QY 5411 CCGAAGGAGAAAGCGGACAGGTATCCGGTAAAGCGGAGCGGTCGGAAACAGAGAGCGCA 5470
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QY 4336 CCGAAGGAGAAAGCGGACAGGTATCCGGTAAAGCGGAGCGGTCGGAAACAGAGAGCGCA 4395
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QY 5471 CGAGGAGGCTTCCAGGGGAAAGCGCTGTATCTTTATAGTCTGTCGGGTTTCGCCACC 5530
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QY 4396 CGAGGAGGCTTCCAGGGGAAAGCGCTGTATCTTTATAGTCTGTCGGGTTTCGCCACC 4455
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QY 4576 TTCTCGGCTATCCCTGATCTCTGTGATACCGGATTAACCGCTTTTGTGCTGAGTGA 4635
Db |||
QY 5711 CGCTCGCGGACGCGAAGCGGACGCGAGCGAGTCACTGAGCGAGGAGCGGAGAGC 5770
Db |||
QY 4636 CGCTCGCGGACGCGAAGCGGACGCGAGCGAGTCACTGAGCGAGGAGCGGAGAGC 4695
Db |||
QY 5771 GCCCAATACGAAACCGCTCTCCCGCGGTTGGCGGATTCATTAATGCGAG 5822
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RESULT 5

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US-09-991-209-35
; Sequence 35, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Philip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; FILE REFERENCE: Expression of Genes Encoding Cell Wall Degrading Enzymes
; CURRENT APPLICATION NUMBER: US/09/991,209
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 4974
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pJ04 vector
US-09-991-209-35
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Query Match 47.5%; Score 2768; DB 10; Length 4974;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2895; Conservative 0; Mismatches 25; Indels 72; Gaps 4;

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Db |||
QY 1833 AAGCAGATCGTTCCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTC 1892
Db |||
QY 2895 TTGCGATGATTATCATATAATTTCTGTGAAATACGTTAAGCATGTAAATAATTAACATGT 2954
Db |||
QY 1893 TTGCGATGATTATCATATAATTTCTGTGAAATACGTTAAGCATGTAAATAATTAACATGT 1952
Db |||
QY 2955 AATGCAATGAGTTATTTATGAGATGGTATTTATGATTAGAGTCCCGCAATTAACATTT 3014
Db |||
QY 1953 AATGCAATGAGTTATTTATGAGATGGTATTTATGATTAGAGTCCCGCAATTAACATTT 2012
Db |||
QY 3015 AATACCGCATAGAAAACAAAATATAGCGCAAACTAGGATAAATTTATCGCGCGCGTGT 3074
Db |||
QY 2013 AATACCGCATAGAAAACAAAATATAGCGCAAACTAGGATAAATTTATCGCGCGCGTGT 2072
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QY 3075 CATCTATGTTACTAGATCGACCTCGAGGATGGGATCCCGCGCGCATGCGACGTCGGGC 3134
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QY 2073 CATCTATGTTACTAGATCGATAGCTTCTAGAGCGCGCGTGGAGC-----T 2119
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QY 3135 CCAATTCGCCCTATAGTGTAGTCTGTTAC---AATCTACGTCGCGTCTTTTACAAAGTC 3191
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QY 2120 CCAATTCGCCCTATAGTGTAGTCTGTTACGCGCGCTACTGCGCGTCTTTTACAAAGTC 2179
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QY 3192 GTGACTGGGAAACCTCGCGTTACCAACTTTAATCGCTTTCAGCACATCCCCCTTTGCG 3251
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QY 2180 GTGACTGGGAAACCTCGCGTTACCAACTTTAATCGCTTTCAGCACATCCCCCTTTGCG 2239
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QY 3252 CCAGCTGGCGTAATAGCAAGAGGCGCGACCGATCGCCCTTCCCAAGTTCGCGAGCC 3311
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QY 2240 CCAGCTGGCGTAATAGCAAGAGGCGCGACCGATCGCCCTTCCCAAGTTCGCGAGCC 2299
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QY 3312 TGAATGGCGAAT- GAGCGGCGCTGTAGCGCGCATTAAGCGCGGCGGTGTGGTTA 3370
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QY 2300 TGAATGGCGAATGGGACGCGCTGTAGCGCGCATTAAGCGCGGCGGTGTGGTTA 2359
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QY 2360 CGCGCAGGTGACCTACACTTCCAGCGCGCTAGCGCGCTCTTTCGCTTTCTTCC 2419
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QY 3431 CTTCTCTTCTCGCCACGTTTCGCCGCTTTCCCGCTCAAGCTCTAAATCGGGGCTCCCTT 3490
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QY 2420 CTTCTCTTCTCGCCACGTTTCGCCGCTTTCCCGCTCAAGCTCTAAATCGGGGCTCCCTT 2479
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QY 2480 TAGGTTCCGATTTAGTGTCTTACGGACCTCGACCGCAAAAACCTTGATTGGGTGATG 2539
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QY 3611 CGTCTTTTAATAGTGTACTCTTGTTCAAAACCTGGAACAACTCAACCTATCTCGGTCT 3670
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QY 2600 CGTCTTTTAATAGTGTACTCTTGTTCAAAACCTGGAACAACTCAACCTATCTCGGTCT 2659
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QY 2660 ATTCTTTGATTATAAGGATTTTCCGATTTTCGGCTATGTTGTTAAAAAATGAGTGA 2719
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QY 3731 TTAAACAAATATTTAAGCGAATTTTAAACAAATATTAAGCTTTTACATTTTCGCTGATG 3790
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QY 2720 TTAAACAAATATTTAAGCGAATTTTAAACAAATATTAAGCTTTTACATTT-----T 2770
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4631 CCCTTCGGCTGGCTGTTTATTGCTGATAAATCTGAGCGGCTGAGCGTGGCTCTCGCG 4690
4632
3588 CCCTTCGGCTGGCTGTTTATTGCTGATAAATCTGAGCGGCTGAGCGTGGCTCTCGCG 3647
4691 GTATCATTTGAGCACTGGGCGCAGATGGTAAGCCCTCCCGTATCGTATGTTTATCTACAG 4750
3648 GTATCATTTGAGCACTGGGCGCAGATGGTAAGCCCTCCCGTATCGTATGTTTATCTACAG 3707
4751 CGGGAGTCCAGGCAACTATGATGAACGAATAGACAGATCGCTGAGATAGTGCCTCAC 4810
3708 CGGGAGTCCAGGCAACTATGATGAACGAATAGACAGATCGCTGAGATAGTGCCTCAC 3767
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3768 TGATTAGCACTGGTACTGTCAGCAAGTTTACTCATATATATCTTATGATGATTTAA 3827
4871 AACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTTTGTATTAATCTCATGACCA 4930
3828 AACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTTTGTATTAATCTCATGACCA 3887
4931 AATTCCTTTAAAGGATCTAGGTGAAGATCCCTTTTGTATTAATCTCATGACCA 4990
3888 AATTCCTTTAAAGGATCTAGGTGAAGATCCCTTTTGTATTAATCTCATGACCA 3947
4991 GATCTCTGAGATCCCTTTTCTGCGGTAATCTGCTGCTGCAAAACAAAAAACAC 5050
3948 GATCTCTGAGATCCCTTTTCTGCGGTAATCTGCTGCTGCAAAACAAAAAACAC 4007
5051 CGTACCAAGCGGTGGTGGTTTGGCGGATCAAGAGTACCAACTCTTTTTCGGAAGTAA 5110
4008 CGTACCAAGCGGTGGTGGTTTGGCGGATCAAGAGTACCAACTCTTTTTCGGAAGTAA 4067
5111 CTGGCTTCAGAGCGGATACCAATATCTGCTCTAGTGTAGCGGTAGTGGCC 5170
4068 CTGGCTTCAGAGCGGATACCAATATCTGCTCTAGTGTAGCGGTAGTGGCC 4127
5171 ACCATCAAGAACTCTGAGCAAGCTTACATCTGCTCTGCTATCTCTGTTTACAG 5230
4128 ACCATCAAGAACTCTGAGCAAGCTTACATCTGCTCTGCTATCTCTGTTTACAG 4187
5231 TGGCTGCTGCCAGTGGCGATAGTCTGTTTACCGGTTGAGTCAAGACGATAGTTAC 5290
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5291 CGGATAAGCGCGGCTGGCTGAAACGGGGGTTGCTGACACAGCCGCTGGAGC 5350
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4308 GAACGACCTTACACCGAACTGAGATACCTACAGCGTGGCTATGAGAAAGCGCCATTC 4367
5411 CGGAAAGGAGAAAGCGGACAGGTATCCGGTAAGCGGAGGTTGGAAACAGGAGCGCA 5470
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5471 CGGAGGAGCTTCAGGGGAAAGCGCTGTTTATGATGCTGCTGCGGTTTCGCCACC 5530
4428 CGGAGGAGCTTCAGGGGAAAGCGCTGTTTATGATGCTGCTGCGGTTTCGCCACC 4487
5531 TCTGATCTGAGCGTCCGATTTTGTGATGCTGCTGAGGGGGGAGGCTATGAAAAACG 5590
4488 TCTGATCTGAGCGTCCGATTTTGTGATGCTGCTGAGGGGGGAGGCTATGAAAAACG 4547
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4668 CCCTTCGGCGCAGCCGAAACGACGAGCGGAGCGAGTCAAGTGAAGGAGGAGGAGGAGG 4727
5771 GCCCAATAGCAAAACCGCTCTCCCGCGGTTGGCGGATTCATTAATGAG 5822
4728 GCCCAATAGCAAAACCGCTCTCCCGCGGTTGGCGGATTCATTAATGAG 4779

RESULT 7
US-09-991-209-33
; Sequence 33, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 5034
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pJQ5 vector
US-09-991-209-33

Query Match 47.5%; Score 2768; DB 10; Length 5034;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2895; Conservative 0; Mismatches 25; Indels 72; Gaps 4;

QY 2835 AAGCAGATCGTTCAAAATTTGGCAATTAAGTTTCTTAAGATTGAATCTGTGGCGGTC 2894
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QY 2895 TTGCGATGATTATCATATAATTTCTGTTGAATTAGTAAAGCATGTAATAATAACATGT 2954
DB 1949 TTGCGATGATTATCATATAATTTCTGTTGAATTAGTAAAGCATGTAATAATAACATGT 2008
QY 2955 AATGATGATGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3014
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QY 3015 AATACGCGATAGAAACAAATATAGCGCGGAAACTAGGATAAATATCGCGCGGTGT 3074
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DB 2356 TGAATGCGCAATGGGACGCGCCCTGTAGCGCGCAATTAAGCGCGGGGTGTGGTGGTTA 2415

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QY 4211 TTGACGCGGCAAGAGCACTCGCTGCGCGCATACATTTCTCAGATGACTTGGTTG 4270
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Db 4161 ACCACTTCAAGAACTCTGTAGCACCGCTACATCTCGCTCTGCTAATCTCTGTTACCAAG 4220
QY 5231 TGGCTGCTGCCAGTGGCGATTAAGTCTGCTTTACCGGCTTGAGCTCAAGAGATAGTTAC 5290
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QY 2150 AGTACTCACCAGTCAAGAAAAGCATCTTACGGATGGCATGACAGTAAGAGAAATATGCA 2209
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QY 4331 GTGCTGCCATAACCATAGTGTATTAACACTGCGGCCAACTTACTTCTGCAACAGATCGGAG 4390
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QY 4391 GACCGAAGAGTAAACCGCTTTTTCACAAACATGGGGATCATGTAATCGCTTGTATC 4450
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QY 4451 GTTGGGAACCGAGCTGAATGAAGCATATACCAACAGCAGCGTGACACCAAGATGCGTG 4510
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QY 4811 TGATTAAAGCATTTGTAATCTGTCAGACCAAGTTTACTCATATATCTTTAGATTGATTAA 4870
Db |||||
QY 4871 AACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCTTTTGTGATAATCTCATGACCA 4930
Db |||||
QY 4931 AAATCCCTTAAGTCACTGTTGTTCCACTGAGCGTACAGCCCGTAGAAAAGATCAAG 4990
Db |||||
QY 4991 GATCTTCTTGAGATCTTTTCTGCGCGTAATCTGCTGTTGCAAAACAAAACACAC 5050
Db |||||
QY 5051 CGCTACCAAGCGTGTGTTTGTGCGGATCAAGAGCTACCAACTCTTTTCCGAAAGTAA 5110
Db |||||
QY 5111 CTGGCTTCAGACAGCGCAGATACCAATCTGCTCTCTAGTGTAGCGGTAGTTAGGCC 5170
Db |||||
QY 5171 ACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCTGCTAATCTCTGTATACAG 5230
Db |||||
QY 5231 TGGCTGCTGCCAGTGGCGATAGTCTGTTTACCGGGTTGGACTCAAGACGATAGTTAC 5290
Db |||||
QY 5291 CGGATAAGCGCAGCGCTGAGCGGGGTTCTGTGACACAGCCCGAGCTTGGAGC 5350
Db |||||
QY 5351 GAAACGACCTACACCGAACTGAGATACCTACAGCGTGTAGCTATGAGAAAGCGCCAGCTTC 5410
Db |||||
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Db 3230 GAACGACCTACACCGAATGAGATACCTACACGGTGAAGTATGAGAAAGCGCCACGCTTC 3289
QY 5411 CCGAAGGGAGAAAGCGGACAGGTATCCGGTAAGCGGCGAGGGTCGGAACAGGAGAGCGCA 5470
Db |||||
QY 5471 CQAGGAGGCTTCCAGGGGGAACCGCTGTGTATCTTTATAGTCTGTCTGCGGTTCGCCACC 5530
Db |||||
QY 5531 TCTGACTTGTAGCGTCTGATTTTGTGATGCTCTGAGGGGGGCGGAGCCCTATGGAAGAACG 5590
Db |||||
QY 5591 CCAGCAACCGCGCTTTTACGGTTCTCGGCTTTTGTGCGCTTTTGTCTACATGTTCT 5650
Db |||||
QY 5651 TTCCTGCGTTATCCCTGATTTCTGTGATAACCGTATTACCGCCCTTTGAGTGAGTGATA 5710
Db |||||
QY 5711 CGCTCGCGCAGCGAAGCGACCGAGCGCAGCGAGTCAAGTGAAGCGAAGCGAAGAGC 5770
Db |||||
QY 5771 GCCCAATACGCAACCGCTCTCCCGCGGCTGTCGCGGATTCATTAATGCGAG 5822
Db |||||
QY 5822 GCCCAATACGCAACCGCTCTCCCGCGGCTGTCGCGGATTCATTAATGCGAG 5870
Db |||||
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RESULT 9

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US-09-991-209-25
; Sequence 25, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Philip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 5277
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pTP5-1 vector
US-09-991-209-25
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Query Match 47.5%; Score 2768; DB 10; Length 5277;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2895; Conservative 0; Mismatches 25; Indels 72; Gaps 4;
QY 2895 AAGCAGATCGTTCAAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTGCGGTC 2894
Db 894 AAGCAGATCGTTCAAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTGCGGTC 953
QY 2895 TTGCGATGATTATCATATAATTTCTGTTGAATTAGTTAAGCATGTAATAATTAACTGT 2954
Db 954 TTGCGATGATTATCATATAATTTCTGTTGAATTAGTTAAGCATGTAATAATTAACTGT 1013
QY 2955 AATCATGACGTTATTTATGAGATGGGTTTTTATGATTAGATCCCGCAATATACATTT 3014
Db 1014 AATCATGACGTTATTTATGAGATGGGTTTTTATGATTAGATCCCGCAATATACATTT 1073
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QY	3015	AATACGGATAGAAAACAAATATAGCGCGCAACTAGGATAAATATATCGCGCGGTGT	3074	QY	4091	TGGGTTACATCGAACTGGATCTCAACAGCGGTAAAGATCCTTGAGAGATTTTCGCCGCCGAAG	4150
Db	1074	AATACGGATAGAAAACAAATATAGCGCGCAACTAGGATAAATATATCGCGCGGTGT	1133	Db	2086	TGGGTTACATCGAACTGGATCTCAACAGCGGTAAAGATCCTTGAGAGATTTTCGCCGCCGAAG	2145
QY	3075	CATCTATGTTACTAGATCGACCTCGACGCGATGGATCCGGCGCGCATGCGAGTCGGGC	3134	QY	4151	AAGGTTTTCAATGATGAGCAGCTTTTAAAGTTCTGCTATGTCGGCGGTATATCCCGTA	4210
Db	1134	CATCTATGTTACTAGATCGATAAGCTTCTAGAGCGCGGTGGAGC-----T	1180	Db	2146	AAGGTTTTCAATGATGAGCAGCTTTTAAAGTTCTGCTATGTCGGCGGTATATCCCGTA	2205
QY	3135	CAAATTCGCCCTATAGTAGTGTATAC---AATTCACGTGGCGGTGTTTTACAAAGTC	3191	QY	4211	TTGACGCGCGGCAAGAGCAACTCGGTCGCGCATACACTATTCTCAGAATGACTTGGTTG	4270
Db	1181	CAAATTCGCCCTATAGTAGTGTATAC---AATTCACGTGGCGGTGTTTTACAAAGTC	1240	Db	2206	TTGACGCGCGGCAAGAGCAACTCGGTCGCGCATACACTATTCTCAGAATGACTTGGTTG	2265
QY	3192	GTGACTGGGAAAACCCCTGGCGTTTACCACACTTAATCGCCTTGAAGCAGATCCGCCCTTTCG	3251	QY	4271	AGTACTCACCAAGTACAGAAAAGATCTTACGGATGGCATGACAGTAAGAGAATATGCA	4330
Db	1241	GTGACTGGGAAAACCCCTGGCGTTTACCACACTTAATCGCCTTGAAGCAGATCCGCCCTTTCG	1300	Db	2266	AGTACTCACCAAGTACAGAAAAGATCTTACGGATGGCATGACAGTAAGAGAATATGCA	2325
QY	3252	CCAGCTGGCGTAATAGCAAGAGAGCCCGCACCGATCGCCCTTCCAAAGTGTGCGAGCC	3311	QY	4331	GTGCTGCCATAACCATGAGTGATAACACTCGGCGCAACTTACTTCTCAGAACGATCGGAG	4390
Db	1301	CCAGCTGGCGTAATAGCAAGAGAGCCCGCACCGATCGCCCTTCCAAAGTGTGCGAGCC	1360	Db	2326	GTGCTGCCATAACCATGAGTGATAACACTCGGCGCAACTTACTTCTCAGAACGATCGGAG	2385
QY	3312	TGATGCGGAT--GGACGCGCCTGTAGCGCGCATTAAGCGCGCGGTGCTGGTGTTA	3370	QY	4391	GACCGAAGGAGCTAAACCGCTTTTTTGGCAACAATGGGGGATCATGTAACTCGCCTTGATC	4450
Db	1361	TGATGCGGAT--GGACGCGCCTGTAGCGCGCATTAAGCGCGCGGTGCTGGTGTTA	1420	Db	2386	GACCGAAGGAGCTAAACCGCTTTTTTGGCAACAATGGGGGATCATGTAACTCGCCTTGATC	2445
QY	3371	CGCGACGCTGACCGCTACACTTGCAGCGCCCTAGCGCCCGCTTTCCTTTCTTCTTC	3430	QY	4451	GTGCGAACCAGAGCTGAATGAAGCCATACAAACGACGAGCGTGACACACGATGCGCTG	4510
Db	1421	CGCGACGCTGACCGCTACACTTGCAGCGCCCTAGCGCCCGCTTTCCTTTCTTCTTC	1480	Db	2446	GTGCGAACCAGAGCTGAATGAAGCCATACAAACGACGAGCGTGACACACGATGCGCTG	2505
QY	3431	CTTCCCTTTTCGCGCACTTTCGCGGCTTTCCCGTCAAGCTCTAAATCGGGGGTCCCTT	3490	QY	4511	TAGCAATGGCAACAAACGCTGCGCAACTATTAACTGCGCAACTTACTTCTAGCTTCCC	4570
Db	1481	CTTCCCTTTTCGCGCACTTTCGCGGCTTTCCCGTCAAGCTCTAAATCGGGGGTCCCTT	1540	Db	2506	TAGCAATGGCAACAAACGCTGCGCAACTATTAACTGCGCAACTTACTTCTAGCTTCCC	2565
QY	3491	TAGGGTCCGATTTAGAGCTTTACGACCTCGACCGCGCAAACTTGATTTGGTGATG	3550	QY	4571	GGCAACAATTAATAGACTGGATGAGCGGGATTAAGTTGCAGGACCACTTCTGCGCTCGG	4630
Db	1541	TAGGGTCCGATTTAGAGCTTTACGACCTCGACCGCGCAAACTTGATTTGGTGATG	1600	Db	2566	GGCAACAATTAATAGACTGGATGAGCGGGATTAAGTTGCAGGACCACTTCTGCGCTCGG	2625
QY	3551	GTTCACTGATGGGCGCATCGCCCTGATAGAGGTTTTTCGCCCTTTGACAGTTGAGTCCA	3610	QY	4631	CCCTTCGCGCTGGCTGTTTTATTGCTGATAAATCTCGAGCGGHTGAGCGGTCTCGCG	4690
Db	1601	GTTCACTGATGGGCGCATCGCCCTGATAGAGGTTTTTCGCCCTTTGACAGTTGAGTCCA	1660	Db	2626	CCCTTCGCGCTGGCTGTTTTATTGCTGATAAATCTCGAGCGGHTGAGCGGTCTCGCG	2685
QY	3611	CGTCTTTAATAGTGGACTTTGTTCACAACTGGAACAACACTCAACCTTATCTCGTCT	3670	QY	4691	GTATCATTCAGCACTGGGCGCGAGATCGTAAGCCCTCCCGTATCGTAGTTATCTACACGA	4750
Db	1661	CGTCTTTAATAGTGGACTTTGTTCACAACTGGAACAACACTCAACCTTATCTCGTCT	1720	Db	2686	GTATCATTCAGCACTGGGCGCGAGATCGTAAGCCCTCCCGTATCGTAGTTATCTACACGA	2745
QY	3671	ATTCTTTTGAATTAAGGATTTTTCGATTTTCGGCTATTGCTTAAATAAGCTGA	3730	QY	4751	CGGCGAGTCAGGCAACTATGATGAACGAATAGACAGATCGCTGAGATAGTGCCTCAC	4810
Db	1721	ATTCTTTTGAATTAAGGATTTTTCGATTTTCGGCTATTGCTTAAATAAGCTGA	1780	Db	2746	CGGCGAGTCAGGCAACTATGATGAACGAATAGACAGATCGCTGAGATAGTGCCTCAC	2805
QY	3731	TTTAAACAAATTTTAAACGCAATTTTAAACAAATATTAAACGTTTTCGCTGATG	3790	QY	4811	TGATTAAGCATTTGGTAACTGTGACAGCAAGTTTACTCATATATATCTTTAGATTGATTA	4870
Db	1781	TTTAAACAAATTTTAAACGCAATTTTAAACAAATATTAAACGTTTTCGCTGATG	1831	Db	2806	TGATTAAGCATTTGGTAACTGTGACAGCAAGTTTACTCATATATATCTTTAGATTGATTA	2865
QY	3791	CGGTAATTTCTCCTTACGCACTGTGCGGATTTTCAACCGCATACAGGTGGCACTTTC	3850	QY	4871	AAATCCCTTAAACGTAAGGATCTAGGTGAAGATCCTTTTGAATCTCTATGACCA	4930
Db	1832	CGGTAATTTCTCCTTACGCACTGTGCGGATTTTCAACCGCATACAGGTGGCACTTTC	1845	Db	2866	AAATCCCTTAAACGTAAGGATCTAGGTGAAGATCCTTTTGAATCTCTATGACCA	2925
QY	3851	GGGAAATGTGCGGGAACCCCTATTGTTTATTTTCTAATATACATTTCAATATGATC	3910	QY	4931	AAATCCCTTAAACGTAAGGATCTAGGTGAAGATCCTTTTGAATCTCTATGACCA	4990
Db	1846	GGGAAATGTGCGGGAACCCCTATTGTTTATTTTCTAATATACATTTCAATATGATC	1905	Db	2926	AAATCCCTTAAACGTAAGGATCTAGGTGAAGATCCTTTTGAATCTCTATGACCA	2985
QY	3911	CGCTCATGAGCAATAACCCCTGATTAATGCTTCAATATAATTGAAAAGGAAGATGA	3970	QY	4991	GATCTTCTTGAGATCCTTTTCTGCGCGTAATCTGCTGCTGTAACAAACCAAC	5050
Db	1906	CGCTCATGAGCAATAACCCCTGATTAATGCTTCAATATAATTGAAAAGGAAGATGA	1965	Db	2986	GATCTTCTTGAGATCCTTTTCTGCGCGTAATCTGCTGCTGTAACAAACCAAC	3045
QY	3971	GTAATTAACATTTCCGTGCGCCCTATTCCCTTTTTCGGCATTTTGCCTTCTGTTT	4030	QY	5051	CGCTACAGCGGTGTTTTGTTGCGGATCAAGAGCTACCAACTCTTTTCCGAAGTAA	5110
Db	1966	GTAATTAACATTTCCGTGCGCCCTATTCCCTTTTTCGGCATTTTGCCTTCTGTTT	2025	Db	3046	CGCTACAGCGGTGTTTTGTTGCGGATCAAGAGCTACCAACTCTTTTCCGAAGTAA	3105
QY	4031	TTGCTCACCCAGAAACGCTGGTGAAGTAAAGATGCTGAAGATCAGTTGGGTGACGAG	4090	QY	5111	CTGCTTTCAGCAGCGCAGATACCAATACTGTCTTCTTAGTGATGCGGTAGTGGCC	5170
Db	2026	TTGCTCACCCAGAAACGCTGGTGAAGTAAAGATGCTGAAGATCAGTTGGGTGACGAG	2085	Db	3106	CTGCTTTCAGCAGCGCAGATACCAATACTGTCTTCTTAGTGATGCGGTAGTGGCC	3165
				QY	5171	ACCACCTCAAGAACTCTGTAGCAGCGGCTACATACCTCGCTCTGCTAATCTGTTTACGAG	5230

Db 3166 ACCACTTCAAGAACTCTGTAGCAGCGCTCATACCTCGCTCTGCTAATCTGTTACAG 3225
Qy TGGCTGCTGCGCAGTGGCGATAGTCTGTCTTACCGGGTTGGACTCAAGACGATGTTAC 5290
Db TGGCTGCTGCGCAGTGGCGATAGTCTGTCTTACCGGGTTGGACTCAAGACGATGTTAC 3285
Qy CGGATAAGGGCGACGGTCTGGGCTGAACGGGGGGTTCGTGCACACAGCCACGCTTGGAGC 5350
Db CGGATAAGGGCGACGGTCTGGGCTGAACGGGGGGTTCGTGCACACAGCCACGCTTGGAGC 3345
Qy GACGACCTACACCGAATCGATGATACCTACAGCTGAGCTATGAGAAAGCGCCACGCTTC 5410
Db GAACGACCTACACCGAATCGATGATACCTACAGCTGAGCTATGAGAAAGCGCCACGCTTC 3405
Qy CCGAAGGGAGAAAGGGCGACAGGTATCCGGTAAAGCGGGGTCGTGCACACAGCCACGCTTC 5470
Db CCGAAGGGAGAAAGGGCGACAGGTATCCGGTAAAGCGGGGTCGTGCACACAGCGAGCGCA 3465
Qy CGAGGGAGCTTCCAGGGGAAACGGCTGTGTATCTTTATAGTCTCTGCGGTTCGCCACC 5530
Db CGAGGGAGCTTCCAGGGGAAACGGCTGTGTATCTTTATAGTCTCTGCGGTTCGCCACC 3525
Qy TCTGACTGAGCTCGATTTTGTGATGCTCGTCAAGGGGGCGAGCCTATGAAAAACG 5590
Db TCTGACTGAGCTCGATTTTGTGATGCTCGTCAAGGGGGCGAGCCTATGAAAAACG 3585
Qy CAGCAACCGGGCTTTTACGGTTCCTGCGCTTTTCTGCGCTTTTCTGCGCTTTTCTGCT 5650
Db CAGCAACCGGGCTTTTACGGTTCCTGCGCTTTTCTGCGCTTTTCTGCGCTTTTCTGCT 3645
Qy TTCTCGGTATCCCTGATTTCTGTGATAACCGTATTAACGGCTTTTGTAGTGAAGTATA 5710
Db TTCTCGGTATCCCTGATTTCTGTGATAACCGTATTAACGGCTTTTGTAGTGAAGTATA 3705
Qy CGCTCGCGCAGCGAAGCAGCGAGCGAGCGAGTCACTGAGCGAGGAAGCGAGAGC 5770
Db CGCTCGCGCAGCGAAGCAGCGAGCGAGCGAGTCACTGAGCGAGGAAGCGAGAGC 3765
Qy GCCCAATAGCAAAACCGCTCTCCCGCGCTTCCCGCGCTTCCCGCGCTTCCCGCGCTTCC 5822
Db GCCCAATAGCAAAACCGCTCTCCCGCGCTTCCCGCGCTTCCCGCGCTTCCCGCGCTTCC 3817

RESULT 10

US-09-991-209-38
; Sequence 38, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 5295
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pUG4 vector
US-09-991-209-38

Query Match 47.5%; Score 2768; DB 10; Length 5295;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2895; Conservative 0; Mismatches 25; Indels 72; Gaps 4;

Qy 2835 AAGCAGATCGTTCAAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCGGTC 2894
Db AAGCAGATCGTTCAAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCGGTC 971
Qy TTGGGATGATATCATATATATTTCTGTGTGAATTCGTTAAGCATGTAAATAAATACATGT 2954
Db TTGGGATGATATCATATATATTTCTGTGTGAATTCGTTAAGCATGTAAATAAATACATGT 1031
Qy AATGCATGAGCTTATTTATGAGATGGCTTTTATGATTAGAGTCCCGCAATTAACATTT 3014
Db AATGCATGAGCTTATTTATGAGATGGCTTTTATGATTAGAGTCCCGCAATTAACATTT 1091
Qy AATAOGCATAGAAAAAATAATATAGCGCAAACTAGGATAAATATTCGCGCGCGTGT 3074
Db AATAOGCATAGAAAAAATAATATAGCGCAAACTAGGATAAATATTCGCGCGCGTGT 1151
Qy CATCTATGTTACTAGATCGACCTGAGGATGGGATCGCGCGCGCATGCGACGTGCGGC 3134
Db CATCTATGTTACTAGATCGATAAGCTTCTAGAGCGCGCGTGGAGC-----T 1198
Qy CCAATTCGCGCTATAGTGTGCTATTAC---AATTACATGCGCGCTGTTTACACGTC 3191
Db CCAATTCGCGCTATAGTGTGCTATTAC---AATTACATGCGCGCTGTTTACACGTC 1258
Qy GTGACTGGGAAAAACCTGCGCTTACCCAACTTAATCGCCTTGACGACATCCCGCTTCG 3251
Db GTGACTGGGAAAAACCTGCGCTTACCCAACTTAATCGCCTTGACGACATCCCGCTTCG 1318
Qy CCAGCTGGCGTAAATAGCGAAGCGCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCC 3311
Db CCAGCTGGCGTAAATAGCGAAGCGCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCC 1378
Qy TGAATGGCGCAAT--GAGACGCGCTGTAGCGCGCATTAAGCGCGCGGTGTTGTTGTTA 3370
Db TGAATGGCGCAAT--GAGACGCGCTGTAGCGCGCATTAAGCGCGCGGTGTTGTTGTTA 1438
Qy CCGCAGCGGTGACCGCTACACTTGGCAGCGCTTACGCGCGCTTTCGCTCTTTCGCTTCC 3430
Db CCGCAGCGGTGACCGCTACACTTGGCAGCGCTTACGCGCGCTTTCGCTCTTTCGCTTCC 1498
Qy CTTCTCTTTCGCGCAGCTTCCCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCTT 3490
Db CTTCTCTTTCGCGCAGCTTCCCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCTT 1558
Qy TAGGTTCCGATTTAGAGCTTTACGCGCCTTACGCGCGCTTTCGCGGTTCGCGGTTCGCTT 3490
Db TAGGTTCCGATTTAGAGCTTTACGCGCCTTACGCGCGCTTTCGCGGTTCGCGGTTCGCTT 1558
Qy GTTACAGTGTGGGCTATCGCCCTGATAGCGGTTCGCGCTTTCGCGGTTCGCGGTTCGCTT 3610
Db GTTACAGTGTGGGCTATCGCCCTGATAGCGGTTCGCGCTTTCGCGGTTCGCGGTTCGCTT 1678
Qy CGTCTTTAATAGTGGACTTGTTCGCGCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCTT 3670
Db CGTCTTTAATAGTGGACTTGTTCGCGCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCTT 1738
Qy ATTCTTTTATTAAGGATTTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCTT 3730
Db ATTCTTTTATTAAGGATTTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCTT 1798
Qy TTTAACAAATATTTAAGCGGAAATTTTAAACAAATATTTAAGCGCTTTCGCGCTTTCGCTT 3790
Db TTTAACAAATATTTAAGCGGAAATTTTAAACAAATATTTAAGCGCTTTCGCGCTTTCGCTT 1849
Qy CGGTATTTTCTCCTTACGATCTGCGGTATTTTCAACCGCATACAGGTGGCGCTTTC 3850
Db CGGTATTTTCTCCTTACGATCTGCGGTATTTTCAACCGCATACAGGTGGCGCTTTC 1863
Qy GGGGAAATGTGCGGAAACCCCTATTGTTTATTTTCTAAATACATTCGCGCTTTC 3910
Db GGGGAAATGTGCGGAAACCCCTATTGTTTATTTTCTAAATACATTCGCGCTTTC 1923

3911 CGCTGATGACAAATACCTGATAAATGCTCAATAATATGAAAGGAGATATGA 3970
1924 CGCTCATGACAAATACCTGATAAATGCTCAATAATATGAAAGGAGATATGA 1983
3971 GTATTCAAAATTTCCGTTGTCGCTTATCCCTTTTTCGGGCAATTTGCTTCTGTTT 4030
1984 GTATTCAAAATTTCCGTTGTCGCTTATCCCTTTTTCGGGCAATTTGCTTCTGTTT 2043
4031 TTGCTCACCCAGAAACGCTGGTGAAGTAAAGTGTGAAGTACAGTGGTGACGAG 4090
2044 TTGCTCACCCAGAAACGCTGGTGAAGTAAAGTGTGAAGTACAGTGGTGACGAG 2103
4091 TGGGTTACATCGAATCGATCTCAACAGCGTGAAGTCTTGAAGTTTTCGCCCGAAG 4150
2104 TGGGTTACATCGAATCGATCTCAACAGCGTGAAGTCTTGAAGTTTTCGCCCGAAG 2163
4151 AACGTTTTCGAATGATGAGCACTTTTAAAGTTCTGCTATGTCGCGCGGTATATCCGCTA 4210
2164 AACGTTTTCGAATGATGAGCACTTTTAAAGTTCTGCTATGTCGCGCGGTATATCCGCTA 2223
4211 TTGACGCGCGGCAAGAGCACTCGGTGCGCGCATACACTATTCTCAGAACTGTTGTTG 4270
2224 TTGACGCGCGGCAAGAGCACTCGGTGCGCGCATACACTATTCTCAGAACTGTTGTTG 2283
4271 AGTACTCACAGTCAAGAAAGCATCTTACGGATGGCATGACAGTAAAGAAATATGCA 4330
2284 AGTACTCACAGTCAAGAAAGCATCTTACGGATGGCATGACAGTAAAGAAATATGCA 2343
4331 GTGCTGCCAATACCAATGATGATAACTGCGGCGCAACTTACTTCTGACAGATCGGAG 4390
2344 GTGCTGCCAATACCAATGATGATAACTGCGGCGCAACTTACTTCTGACAGATCGGAG 2403
4391 GACCGAAGAGTAAACCGCTTTTTCGCAACATCGGGGATCATGTAATCTGCCCTTGATC 4450
2404 GACCGAAGAGTAAACCGCTTTTTCGCAACATCGGGGATCATGTAATCTGCCCTTGATC 2463
4451 GTTGGGAACCGAGCTGAATGAAGCATACCAACGACGAGCGTGACACCAAGTGCCTG 4510
2464 GTTGGGAACCGAGCTGAATGAAGCATACCAACGACGAGCGTGACACCAAGTGCCTG 2523
4511 TAGCAATGGCAACACGTTGCGCAAACTATTAACTGGGGAATCTACTCTAGCTTCCC 4570
2524 TAGCAATGGCAACACGTTGCGCAAACTATTAACTGGGGAATCTACTCTAGCTTCCC 2583
4571 GGCACAAATTAATAGATCGGAGCGGATAAAGTTTCAGAGCACTTCTGCGCTCGG 4630
2584 GGCACAAATTAATAGATCGGAGCGGATAAAGTTTCAGAGCACTTCTGCGCTCGG 2643
4631 CCCTTCCGCTCGCTGTTTATTTGCTGATAAATCTGGAGCGGTGAGCGGTCTCGCG 4690
2644 CCCTTCCGCTCGCTGTTTATTTGCTGATAAATCTGGAGCGGTGAGCGGTCTCGCG 2703
4691 GTATCATTTGACGACTGGGCGCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACCA 4750
2704 GTATCATTTGACGACTGGGCGCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACCA 2763
4751 CGGGAGTCAGGCAACTGATGATGAACAAATAGACAGATCGCTGAGATGGCTCAC 4810
2764 CGGGAGTCAGGCAACTGATGATGAACAAATAGACAGATCGCTGAGATGGCTCAC 2823
4811 TGATTAAGCAATGGTAAGTCTGACCAAGTTTACTCATATATATCTAGATTGATTAA 4870
2824 TGATTAAGCAATGGTAAGTCTGACCAAGTTTACTCATATATATCTAGATTGATTAA 2883
4871 AACTTCATTTTAAATTAAGGATCTAGTGAAGTCTTTTGTGATTAATCTATGACCA 4930
2884 AACTTCATTTTAAATTAAGGATCTAGTGAAGTCTTTTGTGATTAATCTATGACCA 2943
4931 AAATCCCTTAACGAGTCTTTCCTCCACTGAGCGTCAAGCCCGTGAAGAAATCAAG 4990
2944 AAATCCCTTAACGAGTCTTTCCTCCACTGAGCGTCAAGCCCGTGAAGAAATCAAG 3003
4991 GATCTCTTGAGATCTTTTTCCTGCGCGTAAATCTGCTGCTGCAAAACCAACCAAC 5050

3004 GATCTCTTGAGATCTTTTTCCTGCGCGTAAATCTGCTGCTGCAAAACCAACCAAC 3063
5051 CGCTACACGCGGTGTTTGTTCGCGATCAAGAGCTACCACTCTTTTCCGAAGTAA 5110
3064 CGCTACACGCGGTGTTTGTTCGCGATCAAGAGCTACCACTCTTTTCCGAAGTAA 3123
5111 CTGGCTTACAGAGCGGATACCAAACTGCTCTTCTAGTGTAGCGGTAGTTAGGCC 5170
3124 CTGGCTTACAGAGCGGATACCAAACTGCTCTTCTAGTGTAGCGGTAGTTAGGCC 3183
5171 ACCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTCTATCTGTTACAG 5230
3184 ACCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTCTATCTGTTACAG 3243
5231 TGGCTGCTGCGCAGTGGGATGAAGTCTTACCGGGTTGGAATCAAGAGGATAGTTAC 5290
3244 TGGCTGCTGCGCAGTGGGATGAAGTCTTACCGGGTTGGAATCAAGAGGATAGTTAC 3303
5291 CGGATAAGCGGACGCGTGGGCTGAACGGGGGTTCTGCACACAGCCAGCTTGGAGC 5350
3304 CGGATAAGCGGACGCGTGGGCTGAACGGGGGTTCTGCACACAGCCAGCTTGGAGC 3363
5351 GAACGACTTACACCACTGAGATACCTACAGCGTGAATGAGAAAGCCGCTTTC 5410
3364 GAACGACTTACACCACTGAGATACCTACAGCGTGAATGAGAAAGCCGCTTTC 3423
5411 CCGAAGGAGAAAGCGGACAGGTATCCGTTAAGCGGAGGTTCGGAACAGGAGCGCA 5470
3424 CCGAAGGAGAAAGCGGACAGGTATCCGTTAAGCGGAGGTTCGGAACAGGAGCGCA 3483
5471 CGAGGAGCTTCCAGGGGAAACCGCTGATCTTATAGTCTCTGCGGTTTCGCCACC 5530
3484 CGAGGAGCTTCCAGGGGAAACCGCTGATCTTATAGTCTCTGCGGTTTCGCCACC 3543
5531 TCTGACTGAGCTGCTGATTTTGTGATCTGCTCAGGGGGCGGAGCCTATGGAAGAG 5590
3544 TCTGACTGAGCTGCTGATTTTGTGATCTGCTCAGGGGGCGGAGCCTATGGAAGAG 3603
5591 CCAGCAACCGCGCTTTTACGGTTCTGCGCTTTTGTGCTGCTTGTCTCATGTTCT 5650
3604 CCAGCAACCGCGCTTTTACGGTTCTGCGCTTTTGTGCTGCTTGTCTCATGTTCT 3663
5651 TTCCTGCTTATCTGCTGATCTGCTGATTAACCGTATTAACCGCTTGTAGTGAAGTATA 5710
3664 TTCCTGCTTATCTGCTGATCTGCTGATTAACCGTATTAACCGCTTGTAGTGAAGTATA 3723
5711 CGCTCGCGCAGCGCAACGACGCGCAGCGAGTCACTGAGCGAGGAGCGGAAGAGC 5770
3724 CGCTCGCGCAGCGCAACGACGCGCAGCGAGTCACTGAGCGAGGAGCGGAAGAGC 3783
5771 GCCCAATACGCAAAACCGCTCTCCCGCGCTTCCCGCGGATTCATTAATGAG 5822
3784 GCCCAATACGCAAAACCGCTCTCCCGCGCTTCCCGCGGATTCATTAATGAG 3835

RESULT 11
US-09-991-209-27
; Sequence 27, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 5327
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: gTP4a2 vector
US-09-591-209-27

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Query Match	47.5%;	Score 2768;	DB 10;	Length 5327;
Best Local Similarity	96.8%;	Pred. No. 0;		

QY	2835	AAGCAGATCGTTCAAACAATTTGGCAATAAAGATTTCTTAAGATTGAATCCTCTGTCGGCTC	2894
DB	720	AAGCAGATCGTTCAAACAATTTGGCAATAAAGATTTCTTAAGATTGAATCCTCTGTCGGCTC	779
QY	2895	TTGCGATGATTATCATATAAATTTCTGTTGAATTAGTTAAGCATGTATTAATTAACATGT	2954
DB	780	TTGCGATGATTATCATATAAATTTCTGTTGAATTAGTTAAGCATGTATTAATTAACATGT	839
QY	2955	AATGCAATCAGCTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGCAATTATACATTT	3014
DB	840	AATGCAATCAGCTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGCAATTATACATTT	899
QY	3015	AATACGGATAGAAAACAAAATAAGCGCGCAAACTAGGATAAAATATCGCGCGCTGT	3074
DB	900	AATACGGATAGAAAACAAAATAAGCGCGCAAACTAGGATAAAATATCGCGCGCTGT	959
QY	3075	CATCTATGTTACTAGATCGACCTCGAGCATGGGATCCGGCGCGCATCGAGCTCGGGC	3134
DB	960	CATCTATGTTACTAGATCGATAAGCTTCTAGACGGCGCTGGAGC-----T	1006
QY	3135	CCAATTCGCCCTATAGTGAGTCGATTAC--AAATTCAGTCGGCGTCGTTTTACAAGCTC	3191
DB	1007	CCAATTCGCCCTATAGTGAGTCGATTACGGCGCTCAGTCGGCGCTGTTTTACAAGCTC	1066
QY	3192	GTGACTGGGAAAACCCCTGGCGTTACCAACTTAATCGCCTTGACGACATCCCCCTTCG	3251
DB	1067	GTGACTGGGAAAACCCCTGGCGTTACCCAACTTAATCGCCTTGACGACATCCCCCTTCG	1126
QY	3252	CCAGTCGGCGTAATAGCGAAGAGCCCGCACCAATGCGCCTTCCCAACAGTTGCGCAGCC	3311
DB	1127	CCAGTCGGCGTAATAGCGAAGAGCCCGCACCAATGCGCCTTCCCAACAGTTGCGCAGCC	1186
QY	3312	TGAATGGCGAAT--GGACGCGCCCTGTAGCGCGCAATTAAGCGCGCGGCTGTTGTTA	3370
DB	1187	TGAATGGCGAATGGGACGCGCCTGTAGCGCGCAATTAAGCGCGCGGCTGTTGTTA	1245
QY	3371	CGCGCAGCTGACCGCTACACTTGCAGCGCCCTAGCGCCGCTCCCTTTCGCTTCTCC	3430
DB	1247	CGCGCAGCTGACCGCTACACTTGCAGCGCCCTAGCGCCGCTCCCTTTCGCTTCTCC	1306
QY	3431	CTTCCCTTTCGCGCAGTTGCGCGCTTTCCCGTCAAGCTCTAAATCGGGGCTCCCTT	3490
DB	1307	CTTCCCTTTCGCGCAGTTGCGCGCTTTCCCGTCAAGCTCTAAATCGGGGCTCCCTT	1365
QY	3491	TAGGGTTCGATTATAGAGCTTTACGGCACCTCGACCGCAAAAACCTGATTTGGGTGATG	3550
DB	1367	TAGGGTTCGATTATAGAGCTTTACGGCACCTCGACCGCAAAAACCTGATTTGGGTGATG	1426
QY	3551	GTTACGTTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTGGAGTCCA	3610
DB	1427	GTTACGTTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTGGAGTCCA	1486
QY	3611	CGPTCTTTAATAGTGACACTTGTTCCTCAAACTGGAAACAACCTCAACCTATCTCGTCT	3670
DB	1487	CGPTCTTTAATAGTGACACTTGTTCCTCAAACTGGAAACAACCTCAACCTATCTCGTCT	1546
QY	3671	ATTCTTTTGAATTTAAGGGATTTTGGCGATTTTCGGCTTATGGTTAAAAAATGAGCTGA	3730
DB	1547	ATTCTTTTGAATTTAAGGGATTTTGGCGATTTTCGGCTTATGGTTAAAAAATGAGCTGA	1606

QY	3731	TTTAAACAAATTTTAAACGCGAATTTTAAACAAATATTAAACGTTTACAAATTTTCGCTGATG	3790
DB	1607	TTTAAACAAATTTTAAACGCGAATTTTAAACAAATATTAAACGCTTACAAATTT	1657
QY	3791	CGGTATTTCTCCTTACGATCTGTGGGTATTTACACCGCATACAGGTGCGACTTTTC	3850
DB	1658	-----AGTGGCACTTTTC	1671
QY	3851	GGGAAATGTGCGCGGAACCCCTATTGTTTATTATTTCTTAATACATTCAAATATGTATC	3910
DB	1672	GGGAAATGTGCGCGGAACCCCTATTGTTTATTATTTCTTAATACATTCAAATATGTATC	1731
QY	3911	CGCTCATGAGACAATAACCCCTGATPAATGCTTCAATAATATGAAAAAGGAGAGTATGA	3970
DB	1732	CGCTCATGAGACAATAACCCCTGATPAATGCTTCAATAATATGAAAAAGGAGAGTATGA	1791
QY	3971	GTATTCACCAATTTCCGTTGCGCCCTTATCCCTTTTTTGGGCAATTTTGCCTTCTCTGTTT	4030
DB	1792	GTATTCACCAATTTCCGTTGCGCCCTTATCCCTTTTTTGGGCAATTTTGCCTTCTCTGTTT	1851
QY	4031	TTGCTCACCCAGAAAACGCTGGTGAAGATAAAGATGCTGAAGATCAGTTGGTGCACGAG	4090
DB	1852	TTGCTCACCCAGAAAACGCTGGTGAAGATAAAGATGCTGAAGATCAGTTGGTGCACGAG	1911
QY	4091	TGGGTTACATCGAACTGGATCTCAACAGCGGTAAAGATCCTTGAGAGTTTTGCGCCCCGAAG	4150
DB	1912	TGGGTTACATCGAACTGGATCTCAACAGCGGTAAAGATCCTTGAGAGTTTTGCGCCCCGAAG	1971
QY	4151	AAGTTTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGTTGGCGCGTATTAATCCGTA	4210
DB	1972	AAGTTTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGTTGGCGCGTATTAATCCGTA	2031
QY	4211	TTGACGCCGGGCAAGAGCAACTCGGTGCGCGCATACACTATTCTCAGAAAGTCTGTTG	4270
DB	2032	TTGACGCCGGGCAAGAGCAACTCGGTGCGCGCATACACTATTCTCAGAAAGTCTGTTG	2091
QY	4271	AGTACTCACAGTACAGAAAGCATCTTACCGATGGCATGACAGTAAGAGAAATATGCA	4330
DB	2092	AGTACTCACAGTACAGAAAGCATCTTACCGATGGCATGACAGTAAGAGAAATATGCA	2151
QY	4331	GTGCTGCCAATACCATGAGTGATAACACTGCGGCCAATCTTCTGCAACACGATCGGAG	4390
DB	2152	GTGCTGCCAATACCATGAGTGATAACACTGCGGCCAATCTTCTGCAACACGATCGGAG	2211
QY	4391	GACCGAAGAGCTAACCGCTTTTTTGCAAAATGCGGGATCATGTAACCTGCTTGATC	4450
DB	2212	GACCGAAGAGCTAACCGCTTTTTTGCAAAATGCGGGATCATGTAACCTGCTTGATC	2271
QY	4451	GTTGGGAACCGGAGCTGAATGAAGCATACCAAACGAGCGGTGACACACGATCGCTG	4510
DB	2272	GTTGGGAACCGGAGCTGAATGAAGCATACCAAACGAGCGGTGACACACGATCGCTG	2331
QY	4511	TAGCAATGGCAACACGTTGGCAACATTAATTAACCTGCGGAACCTTCTGCGCTCGG	4570
DB	2332	TAGCAATGGCAACACGTTGGCAACATTAATTAACCTGCGGAACCTTCTGCGCTCGG	2391
QY	4571	GGCAACAAATTAATAGACTGGATGGAGCGGATATAAGTTGCAGGACCACTTCTGCGCTCGG	4630
DB	2392	GGCAACAAATTAATAGACTGGATGGAGCGGATATAAGTTGCAGGACCACTTCTGCGCTCGG	2451
QY	4631	CCCTTCGGCTGGCTGTTTATTCGTGATAAATCTGAGCGGTTGAGCGTGGGTCTCGCG	4690
DB	2452	CCCTTCGGCTGGCTGTTTATTCGTGATAAATCTGAGCGGTTGAGCGTGGGTCTCGCG	2511
QY	4691	GTATCAITTCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACAGA	4750
DB	2512	GTATCAITTCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACAGA	2571
QY	4751	CGGGAGTCAGGCAACTATGGATGAAACGAAATAGACAGATCGCTGAGATAGTGCTCAC	4810
DB	2572	CGGGAGTCAGGCAACTATGGATGAAACGAAATAGACAGATCGCTGAGATAGTGCTCAC	2631
QY	4811	TGATTAAGCAATTTGGTAATCTGTCAGCAAGTTTACTCATATATACTTTAGATATGATTTAA	4870

QY	3551	GTTCAGT	AGTGGGCATCGCC	TACATAGACGG	TTTTTCGCC	TTTTCAGCTGGAGTCC	3610
Db	1661	GTTCAGT	AGTGGGCATCGCC	TACATAGACGG	TTTTTCGCC	TTTTCAGCTGGAGTCC	1720
QY	3611	CGTCTCTTA	ATAGTGGAC	TTGTTCC	AACTGG	AAACAAC	3670
Db	1721	CGTCTCTTA	ATAGTGGAC	TTGTTCC	AACTGG	AAACAAC	1780
QY	3671	ATTCTTTT	GATTTAAG	GGGATTTT	CGCGA	TTTTCGGCCTAT	3730
Db	1781	ATTCTTTT	GATTTAAG	GGGATTTT	CGCGA	TTTTCGGCCTAT	1840
QY	3731	TTTAA	CAAAATTTAA	CGGGAATTTT	TAACAA	ATATTAACGTTT	3790
Db	1841	TTTAA	CAAAATTTAA	CGGGAATTTT	TAACAA	ATATTAACGTTT	1891
QY	3791	CGGTATTT	TCTCCTTA	AGCATCTG	TCGGGTATTT	CACACG	3850
Db	1892	CGGTATTT	TCTCCTTA	AGCATCTG	TCGGGTATTT	CACACG	1905
QY	3851	GGGGAAT	TGTCGGG	AACCCCTATTT	GTATTTT	CTAAATACATTT	3910
Db	1906	GGGGAAT	TGTCGGG	AACCCCTATTT	GTATTTT	CTAAATACATTT	1965
QY	3911	CGCTCAT	GAGACA	TAACCTTG	ATAAATGCTT	CAATAATATG	3970
Db	1966	CGCTCAT	GAGACA	TAACCTTG	ATAAATGCTT	CAATAATATG	2025
QY	3971	GTATTTCA	CAATTTCCG	TGTCGCCCTATTT	CCCTTTT	TGCGGCA	4030
Db	2026	GTATTTCA	CAATTTCCG	TGTCGCCCTATTT	CCCTTTT	TGCGGCA	2085
QY	4031	TTGCTCAC	CCGAAACG	TGTTGAA	AGATGCTG	GAAGATCAGT	4090
Db	2086	TTGCTCAC	CCGAAACG	TGTTGAA	AGATGCTG	GAAGATCAGT	2145
QY	4091	TGGGTTA	CTGAACTCA	ACAGCGGT	AAGATCCTT	TGAGAGTTT	4150
Db	2146	TGGGTTA	CTGAACTCA	ACAGCGGT	AAGATCCTT	TGAGAGTTT	2205
QY	4151	AACGTTT	CCAAATCAT	GAGCACTTTT	AAAGTCTG	CTATGTCGCGG	4210
Db	2206	AACGTTT	CCAAATCAT	GAGCACTTTT	AAAGTCTG	CTATGTCGCGG	2265
QY	4211	TTGACG	CGGCGAAG	AGCAACTCG	TGCGCGCATAC	ACTATTTCTCAGA	4270
Db	2266	TTGACG	CGGCGAAG	AGCAACTCG	TGCGCGCATAC	ACTATTTCTCAGA	2325
QY	4271	AGTACTC	ACAGTACAG	AAAGATCTT	ACGATGGC	ATGACAGT	4330
Db	2326	AGTACTC	ACAGTACAG	AAAGATCTT	ACGATGGC	ATGACAGT	2385
QY	4331	GTGCTG	CCATAAC	CATGAGT	ATAACACT	CGCGCAACTT	4390
Db	2386	GTGCTG	CCATAAC	CATGAGT	ATAACACT	CGCGCAACTT	2445
QY	4391	GACCGA	AGGAGCTAA	CCGCTTTTTT	TGCACAA	CATGGGGATCAT	4450
Db	2446	GACCGA	AGGAGCTAA	CCGCTTTTTT	TGCACAA	CATGGGGATCAT	2505
QY	4451	GTTTGG	NAACCGG	AGCTGAATGA	AGCCATAC	CAACGAGCGT	4510
Db	2506	GTTTGG	NAACCGG	AGCTGAATGA	AGCCATAC	CAACGAGCGT	2565
QY	4511	TAGCAAT	TGGCAA	CAACGTTG	CGCAACTATTA	CTGCGCAACT	4570
Db	2566	TAGCAAT	TGGCAA	CAACGTTG	CGCAACTATTA	CTGCGCAACT	2625
QY	4571	GGCAACA	ATTAATAG	ACTTGA	TGGAGGCGG	ATAAGTTG	4630
Db	2626	GGCAACA	ATTAATAG	ACTTGA	TGGAGGCGG	ATAAGTTG	2685
QY	4631	CCCTT	CGGCTG	CTGGTTAT	TGTAFAA	CTTGGAGCGCGG	4690

Db	2686		CCCTTC	CGCGT	CGCTGG	TTTAT	TTGCTG	ATAAT	CTGGAG	CGGTG	AGCGT	GGGTCT	CGCG	2745
Qy	4691	GTATCAT	TTCAGCA	CTGGGG	CCAGAT	GTGTA	AGCCCT	CCCGT	TATCGT	AGTTAT	CTTAC	AGCA	4750	
Db	2746	GTATCAT	TTCAGCA	CTGGGG	CCAGAT	GTGTA	AGCCCT	CCCGT	TATCGT	AGTTAT	CTTAC	AGCA	2805	
Qy	4751	CGGGAGT	CAGCA	ACTATG	GAACG	AAATAG	ACAGAT	CGCTG	AGATAG	GTGCT	CCCTC	AC	4810	
Db	2806	CGGGAGT	CAGCA	ACTATG	GAACG	AAATAG	ACAGAT	CGCTG	AGATAG	GTGCT	CCCTC	AC	2865	
Qy	4811	TGATTA	AGCAT	TGTA	CTGT	CAGAC	CMAGTT	TA	CTCAT	ATAT	TA	CTTTA	GA	4870
Db	2866	TGATTA	AGCAT	TGTA	CTGT	CAGAC	CMAGTT	TA	CTCAT	ATAT	TA	CTTTA	GA	2925
Qy	4871	AAC	TTTCA	TTTTAA	TTTTAA	AAAG	AT	CTAG	GTGA	AGAT	CC	TTTTTG	ATA	4930
Db	2926	AAC	TTTCA	TTTTAA	TTTTAA	AAAG	AT	CTAG	GTGA	AGAT	CC	TTTTTG	ATA	2985
Qy	4931	AAAT	CCCTTAA	CGT	GAGT	TTTC	GT	TCCA	CTGAG	CGGT	CAGAC	CCCGT	AGAAAA	4990
Db	2986	AAAT	CCCTTAA	CGT	GAGT	TTTC	GT	TCCA	CTGAG	CGGT	CAGAC	CCCGT	AGAAAA	3045
Qy	4991	GAT	CTTCT	TGAGAT	CC	TTTTTT	CTG	CGCG	TAAT	CTG	CTG	CTT	G	5050
Db	3046	GAT	CTTCT	TGAGAT	CC	TTTTTT	CTG	CGCG	TAAT	CTG	CTG	CTT	G	3105
Qy	5051	CGCT	ACCAG	CGGT	GGT	TTG	TTG	TGCG	GATCA	CAAG	AGCT	ACCA	AT	5110
Db	3106	CGCT	ACCAG	CGGT	GGT	TTG	TTG	TGCG	GATCA	CAAG	AGCT	ACCA	AT	3165
Qy	5111	CTG	CTT	CAG	CAG	CGC	GAT	ACCA	AT	ACT	CT	CTT	CT	5170
Db	3166	CTG	CTT	CAG	CAG	CGC	GAT	ACCA	AT	ACT	CT	CTT	CT	3225
Qy	5171	ACCA	CTT	CA	GA	AACT	CT	GT	AG	CA	CTG	CT	GT	5230
Db	3226	ACCA	CTT	CA	GA	AACT	CT	GT	AG	CA	CTG	CT	GT	3285
Qy	5231	TGG	CT	GT	CG	CAG	TGG	CGG	AT	AA	GT	CT	T	5290
Db	3286	TGG	CT	GT	CG	CAG	TGG	CGG	AT	AA	GT	CT	T	3345
Qy	5291	CGGA	T	AGG	CG	CA	CGGT	CGGG	CT	GAA	CGGGGG	TT	CT	5350
Db	3346	CGGA	T	AGG	CG	CA	CGGT	CGGG	CT	GAA	CGGGGG	TT	CT	3405
Qy	5351	GA	AG	CA	CT	AC	CG	AACT	GAG	TA	CT	AC	AG	5410
Db	3406	GA	AG	CA	CT	AC	CG	AACT	GAG	TA	CT	AC	AG	3465
Qy	5411	CCGA	AG	GG	GA	AA	AG	CG	CA	GAGT	AT	CCG	GT	5470
Db	3466	CCGA	AG	GG	GA	AA	AG	CG	CA	GAGT	AT	CCG	GT	3525
Qy	5471	CGA	GG	AG	CTT	CA	GGG	GAA	AA	CG	CT	GT	AT	5530
Db	3526	CGA	GG	AG	CTT	CA	GGG	GAA	AA	CG	CT	GT	AT	3585
Qy	5531	TCT	G	A	CTT	G	A	G	CGT	CA	AT	TTTT	T	5590
Db	3586	TCT	G	A	CTT	G	A	G	CGT	CA	AT	TTTT	T	3645
Qy	5591	CCAG	CA	AG	CG	GG	CT	TTTT	T	AC	GGT	TT	CT	5650
Db	3646	CCAG	CA	AG	CG	GG	CT	TTTT	T	AC	GGT	TT	CT	3705
Qy	5651	TT	C	T	C	T	G	A	T	T	C	C	C	5710
Db	3706	TT	C	T	G	A	T	T	C	C	C	C	C	3765
Qy	5711	CCG	T	C	G	C	G	A	G	C	CA	CG	AG	5770

Db 3766 CCGCTCCGCGACGACGACGCGCAGCGAGTCACTGAGCGAGGAGCGGAGGAGC 3825
Qy 5771 GCCCAATACGAAACCGCCTCTCCCGGCGGTTGGCGGATTCATTAATGCAG 5822
Db 3826 GCCCAATACGAAACCGCCTCTCCCGGCGGTTGGCGGATTCATTAATGCAG 3877

RESULT 13
US-09-991-209-23
; Sequence 23, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 5337
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pTP8-5 vector
US-09-991-209-23

Query Match 47.5%; Score 2768; DB 10; Length 5337;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2895; Conservative 0; Mismatches 25; Indels 72; Gaps 4;
Qy 2835 AAGCAGATCGTTCACACATTCGCAATAGGTTCTTAAGATTGAATCCGTTCGCGGTC 2894
Db 954 AAGCAGATCGTTCACACATTCGCAATAGGTTCTTAAGATTGAATCCGTTCGCGGTC 1013
Qy 2895 TTGCGATGATATCATATAATTTCTGTTGAATTAAGATGATGATTAATTAATTAATGAT 2954
Db 1014 TTGCGATGATATCATATAATTTCTGTTGAATTAAGATGATGATTAATTAATTAATGAT 1073
Qy 2955 AATGCAATGATTTATGAGATGGTTTATGATGATGATGATGATGATGATGATGATGATGAT 3014
Db 1074 AATGCAATGATTTATGAGATGGTTTATGATGATGATGATGATGATGATGATGATGATGAT 1133
Qy 3015 AATACGCGATAGAAACAAATATAGCGCAAACTAGGATAAATTAATCGCGCGGTGT 3074
Db 1134 AATACGCGATAGAAACAAATATAGCGCAAACTAGGATAAATTAATCGCGCGGTGT 1193
Qy 3075 CATCTATGTTACTAGATCGACCTCGAGGATGGATCCGCGCGGATGAGATGAGATGAGATGAGAT 3134
Db 1194 CATCTATGTTACTAGATCGATAGCTTCTAGAGCGCGGTGGAGC-----T 1240
Qy 3135 CCAATTCGCCCTATAGTATGATGATTTAC---AATTCATGCGCGGTGTTTACACGTC 3191
Db 1241 CCAATTCGCCCTATAGTATGATGATTTACCGCGCTCCTGCGCGGTGTTTACACGTC 1300
Qy 3192 GTGACTGGGAAACCCCTGGCGTTTACCCAACTTAATCGCCTTGCAGCAGATCCCGCTTCG 3251
Db 1301 GTGACTGGGAAACCCCTGGCGTTTACCCAACTTAATCGCCTTGCAGCAGATCCCGCTTCG 1360
Qy 3252 CCAGCTGGCGTAAATAGCGAAGAGCGCCGAGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGG 3311
Db 1361 CCAGCTGGCGTAAATAGCGAAGAGCGCCGAGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGG 1420
Qy 3312 TGAATGCGGAT--GAGCGCGCTGTAGCGCGCATTAAGCGCGCGGTGTGCGGTTA 3370
Db 1421 TGAATGCGGATGAGCGCGCTGTAGCGCGCATTAAGCGCGCGGTGTGCGGTTA 1480

Qy 3371 CGCGCAGGTGACCGCTACACTTCGCGCGCCTAGCGCGCCTCTTCGCTTCTTCTCC 3430
Db 1481 CGCGCAGGTGACCGCTACACTTCGCGCGCCTAGCGCGCCTCTTCGCTTCTTCTCC 1540
Qy 3431 CTTCTCTTTCGCGCAGCTTCGCGGCTTTCGCGCTCAAGCTCTAAATCGGCGGCTTCTT 3490
Db 1541 CTTCTCTTTCGCGCAGCTTCGCGGCTTTCGCGCTCAAGCTCTAAATCGGCGGCTTCTT 1600
Qy 3491 TAGGTTCCGATTTAGAGCTTTACGCGACCTCGGACCGGATTTTTCGCGCTTTCGCTT 3550
Db 1601 TAGGTTCCGATTTAGAGCTTTACGCGACCTCGGACCGGATTTTTCGCGCTTTCGCTT 1660
Qy 3551 GTTCAGTAGTGGCGCATCGCGCTGATAGAGCTTTTTCGCGCTTTCGCGCTTTCGCTT 3610
Db 1661 GTTCAGTAGTGGCGCATCGCGCTGATAGAGCTTTTTCGCGCTTTCGCGCTTTCGCTT 1720
Qy 3611 CGTCTTTTAAATAGTGGATCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCTT 3670
Db 1721 CGTCTTTTAAATAGTGGATCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCTT 1780
Qy 3671 ATTCTTTTGAATTTAAGGATTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCTT 3730
Db 1781 ATTCTTTTGAATTTAAGGATTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCTT 1840
Qy 3731 TTTAAACAATATTTAAGCGGATTTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCTT 3790
Db 1841 TTTAAACAATATTTAAGCGGATTTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCTT 1891
Qy 3791 CGGTATTTTCTCTTACGATCTGTCGCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCTTTC 3850
Db 1892 -----AGTGGCGACTTTTC 1905
Qy 3851 GGGGAAATGTCGCGGAAACCCCTTATTTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTC 3910
Db 1906 GGGGAAATGTCGCGGAAACCCCTTATTTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTC 1965
Qy 3911 CGCTCATGAGCAATTAACCGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3970
Db 1966 CGCTCATGAGCAATTAACCGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2025
Qy 3971 GTATTCACATTTTCGCTGTCGCGCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCTTTC 4030
Db 2026 GTATTCACATTTTCGCTGTCGCGCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCTTTC 2085
Qy 4031 TTGCTCACCCAGAAACCGCTGTAAGTAAAGATGCTGAGATGCTGAGATGCTGAGATGCTGAGAT 4090
Db 2086 TTGCTCACCCAGAAACCGCTGTAAGTAAAGATGCTGAGATGCTGAGATGCTGAGATGCTGAGAT 2145
Qy 4091 TGGGTTTACATCGAATCGGATCTCAACAGCGGTAAGATCTTTCGAGATGCTTTCGCGCGGAG 4150
Db 2146 TGGGTTTACATCGAATCGGATCTCAACAGCGGTAAGATCTTTCGAGATGCTTTCGCGCGGAG 2205
Qy 4151 AACGTTTTCATGATGAGCATTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTC 4210
Db 2206 AACGTTTTCATGATGAGCATTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCTTTC 2265
Qy 4211 TTGACCGCGGCAAGAGCAATCGCTGCGGATGATGATGATGATGATGATGATGATGATGATGAT 4270
Db 2266 TTGACCGCGGCAAGAGCAATCGCTGCGGATGATGATGATGATGATGATGATGATGATGATGAT 2325
Qy 4271 AGTACTCACAGTCACAGAAAGCAATCTTACGATGATGATGATGATGATGATGATGATGATGAT 4330
Db 2326 AGTACTCACAGTCACAGAAAGCAATCTTACGATGATGATGATGATGATGATGATGATGATGAT 2385
Qy 4331 GTGCTGCTCAATACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4390
Db 2386 GTGCTGCTCAATACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2445
Qy 4391 GACCGAAGAGGATTAACCGCTTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCTT 4450
Db 2446 GACCGAAGAGGATTAACCGCTTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCTT 2505
Qy 4451 GTTGGGAACCGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4510

QY	3192	GTGACTGGGAAACCCCTGGGTTACCCAACTTAATCGCCTTGACGACATCCCCCTTTTCG	Db	2326	AGTACTCACCAGTCACAGAAAGCATCTTACGGATGGCATGACAGTAAGAGAAATATGCA	2385
Db	1301	GTGACTGGGAAACCCCTGGGTTACCCAACTTAATCGCCTTGACGACATCCCCCTTTTCG	QY	4331	GTGCTGCCATTAACCATGAGTGATAACACTTGGGCCAACTTACTTCTGACAAAGATCGGAG	4390
QY	3252	CCAGCTGGGTAATAGGAGAGAGCCCGCACCGATCGCCCTTCCCAACAGTTGGCGAGCC	Db	2386	GTGCTGCCATTAACCATGAGTGATAACACTTGGGCCAACTTACTTCTGACAAAGATCGGAG	2445
Db	1361	CCAGCTGGGTAATAGGAGAGAGCCCGCACCGATCGCCCTTCCCAACAGTTGGCGAGCC	QY	4391	GACCGAAGGAGCTAACCGCTTTTGGTGCACAAATGATGGGGATCATGTAACTCGCCTTGATC	4450
QY	3312	TGAATGGCGAAT - GAGACGCGCCTGTAGCGCGGATTAAGCGCGCGGCGGTGTGTGTTA	Db	2446	GACCGAAGGAGCTAACCGCTTTTGGTGCACAAATGATGGGGATCATGTAACTCGCCTTGATC	2505
Db	1421	TGAATGGCGAATGAGACGCGCCTGTAGCGCGGATTAAGCGCGCGGCGGTGTGTGTTA	QY	4451	GTTGGGAAACCGAGCTGAATGAAGCATACCAACAGAGCGGTGACACCAAGATGCGCTG	4510
QY	3371	CGCGAGCGTGACCGCTACACTTGCAGCGCCCTAGCGCCGCTCTCTTTCGCTTCTTCTCC	Db	2506	GTTGGGAAACCGAGCTGAATGAAGCATACCAACAGAGCGGTGACACCAAGATGCGCTG	2565
Db	1481	CGCGAGCGTGACCGCTACACTTGCAGCGCCCTAGCGCCGCTCTCTTTCGCTTCTTCTCC	QY	4511	TAGCAATGGCAACCAACGTTTGGCGAACTTAATTAATGGCGAACTTAACTCTCTAGCTTCC	4570
QY	3431	CTTCTCTTCTCGCCAGCTTTCGCGGCTTTCGCCGCTTTCGCCGCTTTCGCCGCTTTC	Db	2566	TAGCAATGGCAACCAACGTTTGGCGAACTTAACTTAATGGCGAACTTAACTCTCTAGCTTCC	2625
Db	1541	CTTCTCTTCTCGCCAGCTTTCGCGGCTTTCGCCGCTTTCGCCGCTTTCGCCGCTTTC	QY	4571	GGCAACAATTAATAGACTGGATGGAGGGCGGATAAAGTTGCGAGGACCTTCTGCGCTCGG	4630
QY	3491	TAGGTTCCGATTTAGAGCTTTACGGGACCTCGACCGGAAACCTTGAATTTGGGTGATG	Db	2626	GGCAACAATTAATAGACTGGATGGAGGGCGGATAAAGTTGCGAGGACCTTCTGCGCTCGG	2685
Db	1601	TAGGTTCCGATTTAGAGCTTTACGGGACCTCGACCGGAAACCTTGAATTTGGGTGATG	QY	4631	CCCTTCGCGCTGGCTGTTTATTGCTGATAAATCTGGAGCCGCTGAGCGTGGGTCTCGCG	4690
QY	3551	GTTACGTTAGTGGGCGCATCGCCCTGATAGACGGTTTTCGCCCTTTCGAGTTGGAGTCCA	Db	2686	CCCTTCGCGCTGGCTGTTTATTGCTGATAAATCTGGAGCCGCTGAGCGTGGGTCTCGCG	2745
Db	1661	GTTACGTTAGTGGGCGCATCGCCCTGATAGACGGTTTTCGCCCTTTCGAGTTGGAGTCCA	QY	4691	GTATCAITTCGACACTGGGCGCAGATGTTAAGCCCTCCGCTATCTAGTATCTACAGCA	4750
QY	3611	CGTCTCTTAATAGTGGACTCTTGTTCCAAACCTGGAACACACATCAACCCCTATCTCGGT	Db	2746	GTATCAITTCGACACTGGGCGCAGATGTTAAGCCCTCCGCTATCTAGTATCTACAGCA	2805
Db	1721	CGTCTCTTAATAGTGGACTCTTGTTCCAAACCTGGAACACACATCAACCCCTATCTCGGT	QY	4751	CGGGAGTTCAGGCAACTATGATGATGACGAAATAGACAGATCGCTGATAGTGGCTCAC	4810
QY	3671	ATTCTTTTCAATTAAGGATTTTCCGCAATTCGCGCTTATGGTTAAAAATGAGCTCA	Db	2806	CGGGAGTTCAGGCAACTATGATGATGACGAAATAGACAGATCGCTGATAGTGGCTCAC	2865
Db	1781	ATTCTTTTCAATTAAGGATTTTCCGCAATTCGCGCTTATGGTTAAAAATGAGCTCA	QY	4811	TGATTAAGCATTTGTTAAATTTAAAGGATCTAGTGAAGATCTTTTGTGATTAATTA	2925
QY	3731	TTTAAACAATATTTAAGCGAATTTTAAACAATATTTAACAATATTTAACAATTT	Db	4871	AACTTCATTTTAAATTTAAAGGATCTAGTGAAGATCTTTTGTGATTAATTA	4930
Db	1841	TTTAAACAATATTTAAGCGAATTTTAAACAATATTTAACAATATTTAACAATTT	QY	2926	AACTTCATTTTAAATTTAAAGGATCTAGTGAAGATCTTTTGTGATTAATTA	2985
QY	3791	CGGTATTTCTCTTACGATCTGTGCGGTATTTTCAACCGCATACAGGTGGCACTTTTC	Db	4931	AAATCCCTTAAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCGCTAGAAAGATCAAG	4990
Db	1892	-----AGGTGGCACTTTTC	QY	2986	AAATCCCTTAAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCGCTAGAAAGATCAAG	3045
QY	3851	GGGAAATGTCGCGGAAACCCCTATTGTTTATTTTCTTAATATGATTAATGATC	Db	4991	GATCTTCTGAGATCTTTTTCGCGTAACTCTGCTGCTTTCGCAACAAAAAACCCAC	5050
Db	1906	GGGAAATGTCGCGGAAACCCCTATTGTTTATTTTCTAAATACATTTCAATGATC	QY	3046	GATCTTCTGAGATCTTTTTCGCGTAACTCTGCTGCTTTCGCAACAAAAAACCCAC	3105
QY	3911	CGCTCATGACAAATACCCCTGATAAATGCTTCAATAATTTGAAAGGAGAGATGA	Db	5051	CGCTACAGCGGTGGTTGTTTCCCGGATCAAGAGTACCAACTCTTTTTCGAGGTAA	5110
Db	1966	CGCTCATGACAAATACCCCTGATAAATGCTTCAATAATTTGAAAGGAGAGATGA	QY	3106	CGCTACAGCGGTGGTTGTTTCCCGGATCAAGAGTACCAACTCTTTTTCGAGGTAA	3165
QY	3971	GTATTCACAAATTTCCGTGTCGCCCTTATTCCTTTTTCGCGCAATTTTGCCTCTTTT	Db	5111	CTGGCTTCAGACAGCGCAGATACCAAAATCTGCTTCTCTAGTACCGCTAGTGGCC	3225
Db	2026	GTATTCACAAATTTCCGTGTCGCCCTTATTCCTTTTTCGCGCAATTTTGCCTCTTTT	QY	3166	CTGGCTTCAGACAGCGCAGATACCAAAATCTGCTTCTCTAGTACCGCTAGTGGCC	3285
QY	4031	TTGCTCACCCAGAAACCCCTGTTGAAGTAAAGATGCTGAAGATCAGTTGGTGCACGAG	Db	5171	ACCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTGCTCTAATCTGTTACAG	5230
Db	2086	TTGCTCACCCAGAAACCCCTGTTGAAGTAAAGATGCTGAAGATCAGTTGGTGCACGAG	QY	3226	ACCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTGCTCTAATCTGTTACAG	5290
QY	4091	TGGGTTACATCGAATCGATCTCAACAGCGGTAAAGATCTTTCGAGAGTTTTCGCCCCGAG	Db	5231	TGGCTGCTGCCAGTGGCGATAAGTCTGTTTACCGGGTTGGATCTCAAGAGATAGTTAC	3345
Db	2146	TGGGTTACATCGAATCGAATCGAATCTCAACAGCGGTAAAGATCTTTCGAGAGTTTTC	QY	3286	TGGCTGCTGCCAGTGGCGATAAGTCTGTTTACCGGGTTGGATCTCAAGAGATAGTTAC	3350
QY	4151	AACGTTTTTCAATGATGACACTTTTAAAGTTCTGATGTTGGCGCGGTATATCCCGTA	Db	5291	CGGATAAGGCGCAGCGCTCGGCTGAACGGGGGTTTCTGTCACACAGCCAGCTTGGAGC	3405
Db	2206	AACGTTTTTCAATGATGACACTTTTAAAGTTCTGATGTTGGCGCGGTATATCCCGTA	QY	3346	CGGATAAGGCGCAGCGCTCGGCTGAACGGGGGTTTCTGTCACACAGCCAGCTTGGAGC	3410
QY	4211	TTGACGCGCGGACAGAGCACTCGGTCCGCCATACACTATTTCTCAGAACTGCTTGGTTG	Db	5351	GAAACGACTACACCGAACTGAGATACCTTACAGCGGTGAGCTATGAGAAAGCGGCTTC	5410
Db	2266	TTGACGCGCGGACAGAGCACTCGGTCCGCCATACACTATTTCTCAGAACTGCTTGGTTG	QY			
QY	4271	AGTACTCACCAGTCACAGAAAGCATCTTACGGATGGCATGACAGTAAGAGAAATATGCA				

Db 3406 GAACGACCTACACCGAACTGAGATACCTACAGCGTGTAGCTATGAGAAAGCCACGGCTTC 3465
Qy CCGAAGGAGAAAGCGGACAGGTATCCGTAAGCGGCGAGGTCGGAACAGAGAGCGCA 5470
Db CCGAAGGAGAAAGCGGACAGGTATCCGTAAGCGGCGAGGTCGGAACAGAGAGCGCA 3525
Qy CGAGGAGCTTCCAGGGGAAACCGCTGTGTATCTTTATAGTCCCTGTGGGTTTCGCCACC 5530
Db CGAGGAGCTTCCAGGGGAAACCGCTGTGTATCTTTATAGTCCCTGTGGGTTTCGCCACC 3585
Qy TCTGACGTGAGCGTCGATTTTGTGATGCTCGTCAGGGGGCGAGGCTATGGAAGAAACG 5590
Db TCTGACGTGAGCGTCGATTTTGTGATGCTCGTCAGGGGGCGAGGCTATGGAAGAAACG 3645
Qy CCAGCAACGGCGGCTTTTACGGTTCTCGGCTTTTGTGATGCTCGTCAGGGGGCGAGGCTATGGAAGAAACG 5591
Db CCAGCAACGGCGGCTTTTACGGTTCTCGGCTTTTGTGATGCTCGTCAGGGGGCGAGGCTATGGAAGAAACG 5650
Qy 3646 CCAGCAACGGCGGCTTTTACGGTTCTCGGCTTTTGTGATGCTCGTCAGGGGGCGAGGCTATGGAAGAAACG 3705
Qy 5651 TTCTGCGTTATCCCTGATTTCTGTGATAACCGTATTAACCGCTTTTGTGATGAGTGTGATA 5710
Db TTCTGCGTTATCCCTGATTTCTGTGATAACCGTATTAACCGCTTTTGTGATGAGTGTGATA 3765
Qy CCGCTCCCGCAGCGCAACCGAGCGAGCGAGTCACTGAGCGAGGAGCGAGGAGCGAGC 5770
Db CCGCTCCCGCAGCGCAACCGAGCGAGCGAGTCACTGAGCGAGGAGCGAGGAGCGAGC 3825
Qy 5771 GCCCAATACCAACCGCTCTCCCGCGGTTGGCGGATTCATTATGCGAG 5822
Db 3826 GCCCAATACCAACCGCTCTCCCGCGGTTGGCGGATTCATTATGCGAG 3877

RESULT 15

US-09-991-209-15
; Sequence 15, Application US/09991209
; Publication No. US20030024009A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Langdon, Timothy
; APPLICANT: Morse, Phillip
; TITLE OF INVENTION: Manipulation of the Phenolic Acid
; TITLE OF INVENTION: Content and Digestibility of Plant Cell Walls by Targeted
; TITLE OF INVENTION: Expression of Genes Encoding Cell Wall Degrading Enzymes
; FILE REFERENCE: GC648-2
; CURRENT APPLICATION NUMBER: US/09/991,209
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/249,608
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 5338
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pTF10-1 vector
US-09-991-209-15

Query Match 47.5%; Score 2768; DB 10; Length 5338;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2895; Conservative 0; Mismatches 25; Indels 72; Gaps 4;
Qy 2835 AAGCAGATCGTTCAACACATTTGGCAATAAGTTTCTTAAGATTGAATCCTGTGGCGGTC 2894
Db 955 AAGCAGATCGTTCAACACATTTGGCAATAAGTTTCTTAAGATTGAATCCTGTGGCGGTC 1014
Qy 2895 TTGCGATGATTATCATATTAATTTCTGTTGAATTAACGTTAAGCATGTAATAATTAACATGT 2954
Db 1015 TTGCGATGATTATCATATTAATTTCTGTTGAATTAACGTTAAGCATGTAATAATTAACATGT 1074
Qy 2955 AATGATACGTTATTTATGATGAGTGGTTTATGATTAAGTCCCGCAATTAACATTT 3014
Db 1075 AATGATACGTTATTTATGATGAGTGGTTTATGATTAAGTCCCGCAATTAACATTT 1134

Qy 3015 AATACGCGATAGAAAAAATAATATAGCGCGCAAACTAGGATAAAATATATCGCGCGCGGTGT 3074
Db 1135 AATACGCGATAGAAAAAATAATATAGCGCGCAAACTAGGATAAAATATATCGCGCGCGGTGT 1194
Qy 3075 CATCTATGTTACTAGATCGACCTCGAGCATGCGGATCGCGCGCGCATGCGACGTGCGGC 3134
Db 1195 CATCTATGTTACTAGATCGATAAGCTTCTAGAGCGCGCGGTGAGC-----T 1241
Qy 3135 CCAATTCGCCCTATAGTGAGTCTGATTAC---AATTCATCGGCCGTGTTTAAACAGTC 3191
Db 1242 CCAATTCGCCCTATAGTGAGTCTGATTACCGGCGCTCACTGGCGGTGTTTAAACAGTC 1301
Qy 3192 GTGACTGGGAAAAACCTTGGCGTTACCCAACTTAATTCGCTTTCAGACATATCCCTTTTCG 3251
Db 1302 GTGACTGGGAAAAACCTTGGCGTTACCCAACTTAATTCGCTTTCAGACATATCCCTTTTCG 1361
Qy 3252 CCAGCTCGGCTTAATAGGAAAGAGCGCGCATCGGATCGGCTTCCCAACAGTTGCGAGCC 3311
Db 1362 CCAGCTCGGCTTAATAGGAAAGAGCGCGCATCGGATCGGCTTCCCAACAGTTGCGAGCC 1421
Qy 3312 TGAATGCGCAAT-GGACGCGCCCTGTAGCGGCGCATTAAGCGGCGGCGGTGTGTTGTTA 3370
Db 1422 TGAATGCGCAATGGAGCGCCCTGTAGCGGCGCATTAAGCGGCGGCGGTGTGTTGTTA 1481
Qy 3371 CGCGGAGCGTACCGCTACCTTGGCGGCGCTAGCGCGGCTTCTTTCGCTTTCTTC 3430
Db 1482 CGCGGAGCGTACCGCTACCTTGGCGGCGCTAGCGCGGCTTCTTTCGCTTTCTTC 1541
Qy 3431 CTTCCTTTCTCGCCAGCTTCCCGGCTTCCCGCTCAAGCTCAAAATCGGCGGCTCCCTT 3490
Db 1542 CTTCCTTTCTCGCCAGCTTCCCGGCTTCCCGCTCAAGCTCAAAATCGGCGGCTCCCTT 1601
Qy 3491 TAGGTTTCGATTTAGAGCTTTACGCGACCTCGACCGCAAAATCTGATTGGGTGATG 3550
Db 1602 TAGGTTTCGATTTAGTGTCTTACGCGACCTCGACCGCAAAATCTGATTGGGTGATG 1661
Qy 3551 GTTCAGTGTGGGCGCATCGCCCTGATAGACGTTTTTTCGCCCTTTGACGTTGAGTCCA 3610
Db 1662 GTTCAGTGTGGGCGCATCGCCCTGATAGACGTTTTTTCGCCCTTTGACGTTGAGTCCA 1721
Qy 3611 CGTTCTTTAATAGTGACCTTGTTCGCAACCTGGAACACACTCAACCTTATCGGTCT 3670
Db 1722 CGTTCTTTAATAGTGACCTTGTTCGCAACCTGGAACACACTCAACCTTATCGGTCT 1781
Qy 3671 ATTCTTTGATTTAAGGGATTTTTCGCGATTTTCGCGCTATTGTTAAATAATGAGCTGA 3730
Db 1782 ATTCTTTGATTTAAGGGATTTTTCGCGATTTTCGCGCTATTGTTAAATAATGAGCTGA 1841
Qy 3731 TTTAACAATATTTAAGCGGAATTTTAAACAATATTAACGTTTAAATTCGCTGATG 3790
Db 1842 TTTAACAATATTTAAGCGGAATTTTAAACAATATTAACGTTTAAATTCGCTGATG 1892
Qy 3791 CGGTATTTTCTCTTACGCACTGTGCGGATTTTTCACCGCATACAGTGGCACTTTTC 3850
Db 1893 -----AGTGGCACTTTTC 1906
Qy 3851 GGGGAAATGTGCGCGAACCCTTATTTGTTTATTTTCTAAATACATTCAAATATGTATC 3910
Db 1907 GGGGAAATGTGCGCGAACCCTTATTTGTTTATTTTCTAAATACATTCAAATATGTATC 1966
Qy 3911 CGTCAATGAGCAATTAACCTGATAAATGCTTCAATAATATTGAAAAAGGAGATGA 2026
Db 1967 CGTCAATGAGCAATTAACCTGATAAATGCTTCAATAATATTGAAAAAGGAGATGA 2086
Qy 3971 GTATTCAACATTTCCGTGCGCCCTTATTCCTTTTTCGCGCATTTTTCCTTCTGTTT 4030
Db 2027 GTATTCAACATTTCCGTGCGCCCTTATTCCTTTTTCGCGCATTTTTCCTTCTGTTT 2086
Qy 4031 TTGCTCACCCAGAAACCGTGTGAAAGTAAAGATGCTGAAGATCAGTTGGGTGCGACGAG 4090
Db 2087 TTGCTCACCCAGAAACCGTGTGAAAGTAAAGATGCTGAAGATCAGTTGGGTGCGACGAG 2146
Qy 4091 TGGGTTATCATCGAACTGGATCTCAACAGCGGTAAAGATCTTTGAGAGTTTTCGCCCGGAG 4150

Db 2147 TGGGTTATCATGAACTGATCTCAACAGCGTAAAGTCTTGGAGTTTTCGCCCGGAG 2206
Qy
4151 AACGTTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGCGGCGGTTATTTCCCGTA 4210
Db 2207 AACGTTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGCGGCGGTTATTTCCCGTA 2266
Qy 4211 TTGAGCGCGGCAAGAGCAACTCGGTCCGCCATACACTATTTCTCAGAACTGACTTGGTTG 4270
Db 2267 TTGAGCGCGGCAAGAGCAACTCGGTCCGCCATACACTATTTCTCAGAACTGACTTGGTTG 2326
Qy 4271 AGTACTCACCAGTACAGAAAGCACTTACGAGTGGCATGACAGTAAAGAAATTTATGCA 4330
Db 2327 AGTACTCACCAGTACAGAAAGCACTTACGAGTGGCATGACAGTAAAGAAATTTATGCA 2386
Qy 4331 GTGCTGCCATAACCATGAGTGATTAACATGCGGCCAACTTACTTCTGACACGATCGGAG 4390
Db 2387 GTGCTGCCATAACCATGAGTGATTAACATGCGGCCAACTTACTTCTGACACGATCGGAG 2446
Qy 4391 GACCGAAGAGTAAACCGCTTTTTCACAACTGGGGATCATTAACCTGCGCTTGATC 4450
Db 2447 GACCGAAGAGTAAACCGCTTTTTCACAACTGGGGATCATTAACCTGCGCTTGATC 2506
Qy 4451 GTTGGCAACCGAGCTGAATGAAGCCATACCAACGACGAGCGTGACACCAAGATGCGTG 4510
Db 2507 GTTGGCAACCGAGCTGAATGAAGCCATACCAACGACGAGCGTGACACCAAGATGCGTG 2566
Qy 4511 TAGCAATGGCAACAAAGTTGCGCAACTTAACTTAACTGGCGAACTTACTTCTAGCTTCCC 4570
Db 2567 TAGCAATGGCAACAAAGTTGCGCAACTTAACTTAACTGGCGAACTTACTTCTAGCTTCCC 2626
Qy 4571 GGCACAAATTAATAGACTGGAGCGGATGAAAGTTTCAGACCACTTCTGCGCTCGG 4630
Db 2627 GGCACAAATTAATAGACTGGAGCGGATGAAAGTTTCAGACCACTTCTGCGCTCGG 2686
Qy 4631 CCCTTCCGCGCTGGCTGTTTATTTGCTGATAAATCTGGAGCGGATGAGCGTCTGCGG 4690
Db 2687 CCCTTCCGCGCTGGCTGTTTATTTGCTGATAAATCTGGAGCGGATGAGCGTCTGCGG 2746
Qy 4691 GTATCATTTGAGCACTGGGCGGAGATGTTAAGCCCTCCCGTATCTATCTACACCA 4750
Db 2747 GTATCATTTGAGCACTGGGCGGAGATGTTAAGCCCTCCCGTATCTATCTACACCA 2806
Qy 4751 CGGGAGTCAAGCACTATGATGACGAAATAGACAGATCGTGAAGATGAGTGCCTCAC 4810
Db 2807 CGGGAGTCAAGCACTATGATGACGAAATAGACAGATCGTGAAGATGAGTGCCTCAC 2866
Qy 4811 TGATTAAGCAATGGTAACTGTACAGCAAGTTTACTCATATATATCTTTAGATTTAA 4870
Db 2867 TGATTAAGCAATGGTAACTGTACAGCAAGTTTACTCATATATATCTTTAGATTTAA 2926
Qy 4871 AACTTCATTTTAAATTAAGGATCTAGTGAAGATCCTTTTGGATTAATCTCATGACCA 4930
Db 2927 AACTTCATTTTAAATTAAGGATCTAGTGAAGATCCTTTTGGATTAATCTCATGACCA 2986
Qy 4931 AAATCCCTTAAAGTGGTTTTCCTCCAGTGGCTCAGACCCCGTAGAAAAGATCAAG 4990
Db 2987 AAATCCCTTAAAGTGGTTTTCCTCCAGTGGCTCAGACCCCGTAGAAAAGATCAAG 3046
Qy 4991 GATCTTCTTGAGATCCTTTTCTGCGGTAATCTGCTGCTGCAAAACCAAAACCCAC 5050
Db 3047 GATCTTCTTGAGATCCTTTTCTGCGGTAATCTGCTGCTGCAAAACCAAAACCCAC 3106
Qy 5051 CGCTACAGCGGTTGTTTGGCGGATCAAGGATCAACACTCTTTTTCGGAAGTAA 5110
Db 3107 CGCTACAGCGGTTGTTTGGCGGATCAAGGATCAACACTCTTTTTCGGAAGTAA 3166
Qy 5111 CTGCTTTCAGCAGAGCGCAGATACCAATATCTGCTTCTAGTGTAGCCGTAGTTAGGCC 5170
Db 3167 CTGCTTTCAGCAGAGCGCAGATACCAATATCTGCTTCTAGTGTAGCCGTAGTTAGGCC 3226
Qy 5171 ACCACTTCAAGAACTCTGTAGCAGCGGCTCATACCTGCTCTGCTAATCTGTTACCAG 5230

Db 3227 ACCACTTCAAGAACTCTGTAGCAGCGCTACATACCTCGCTCTGCTAATCTGTTACCAG 3286
Qy 5231 TGGCTGTGTCAGTGGCGATAAGTCGTCTTTTACCGGTTGGACTCAAGAGATAGTTAC 5290
Db 3287 TGGCTGTGTCAGTGGCGATAAGTCGTCTTTTACCGGTTGGACTCAAGAGATAGTTAC 3346
Qy 5291 CGGATAAGGCGCAGCGGTGCGGCTGAACCGGGGGTTCGTGCACACAGCCAGCTTGGAGC 5350
Db 3347 CGGATAAGGCGCAGCGGTGCGGCTGAACCGGGGGTTCGTGCACACAGCCAGCTTGGAGC 3406
Qy 5351 GAAAGCACTACACCGAACTGAGATACCTTACAGCGTGAAGTATGAGAAAGCGCCAGCTTC 5410
Db 3407 GAAAGCACTACACCGAACTGAGATACCTTACAGCGTGAAGTATGAGAAAGCGCCAGCTTC 3466
Qy 5411 CCGAAGGAGAAAGCGGACAGGTATCCGTTAAGCGGCGAGGTCGGAACAGGAGCGCA 5470
Db 3467 CCGAAGGAGAAAGCGGACAGGTATCCGTTAAGCGGCGAGGTCGGAACAGGAGCGCA 3526
Qy 5471 CGAGGAGCTTCCAGGGGAAACCGCTGCTGATCTTATAGTCTCTGCGGTTTCGCCACC 5530
Db 3527 CGAGGAGCTTCCAGGGGAAACCGCTGCTGATCTTATAGTCTCTGCGGTTTCGCCACC 3586
Qy 5531 TCTGACTTGAAGCTCGATTTTGTGATGCTGCTCAGGGGGCGGAGCCTATGAAAAAGC 5590
Db 3587 TCTGACTTGAAGCTCGATTTTGTGATGCTGCTCAGGGGGCGGAGCCTATGAAAAAGC 3646
Qy 5591 CCAGCAACCGGCGCTTTTACGGTTCCCTGGCTTTTGTGGCTTTTGTCTCATATGTTCT 5650
Db 3647 CCAGCAACCGGCGCTTTTACGGTTCCCTGGCTTTTGTGGCTTTTGTCTCATATGTTCT 3706
Qy 5651 TTCTGCGTTATCCCTGATCTGATGATTAACCGTATTAACCGCTTTTGTAGTGAAGTATA 5710
Db 3707 TTCTGCGTTATCCCTGATCTGATGATTAACCGTATTAACCGCTTTTGTAGTGAAGTATA 3766
Qy 5711 CCGCTCGCGCAGCCGAAACGACCGAGCGCAGGAGTCACTGAGCGAGGAAAGCGAAGC 5770
Db 3767 CCGCTCGCGCAGCCGAAACGACCGAGCGCAGGAGTCACTGAGCGAGGAAAGCGAAGC 5822
Qy 5771 GCCCAATACGAAACCGCTCTCCCGCGCTTGGCCGATTCATTAATGAG 5878
Db 3827 GCCCAATACGAAACCGCTCTCCCGCGCTTGGCCGATTCATTAATGAG 3878

Search completed: June 21, 2004, 21:59:55
Job time : 1571 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2004, 13:47:23 ; Search time 8916 Seconds
(without alignments)
19499.508 Million cell updates/sec

Title: US-09-924-197-1

Perfect score: 5822

Sequence: 1 ctggcagcaggtttcccg.....tggccgattcattgacgag 5822

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estnu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_nam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_fod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gsl:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	1055.8	18.1	1070	9	AJ281552
2	986.4	16.9	1013	12	BM438846
3	924	15.9	1004	9	AJ281480
4	916.2	15.7	973	14	CD458281

5	885.6	15.2	917	14	CD458286
6	873	15.0	935	12	BG838279
7	865.4	14.9	918	14	CD459092
8	841	14.4	841	9	AL042026
9	832.8	14.3	872	14	CD459085
c 10	825	14.2	1073	14	CF289652
11	824.6	14.2	854	12	BM438950
12	819.6	14.1	870	14	CD458333
c 13	815.6	14.0	1249	28	BZ572284
14	814.4	14.0	1126	28	BZ577702
15	808	13.9	819	14	CD649375
c 16	807.6	13.9	966	28	BZ570738
17	801.6	13.8	1483	28	BZ575896
18	797.6	13.7	1011	28	BZ576726
c 19	785.4	13.5	1574	28	BZ572566
c 20	777.8	13.4	800	9	AJ281449
21	777.6	13.4	910	14	CD649387
22	774.8	13.3	1336	28	BZ575810
23	774.4	13.3	789	14	CD280920
c 24	772.4	13.3	954	9	AL044364
c 25	771.8	13.3	1067	9	AU081137
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27	763.2	13.1	780	13	BQ825693
28	757	13.0	759	14	CD279661
29	755.4	13.0	1483	28	BZ571475
30	753.6	12.9	797	12	BM410796
31	745.4	12.8	786	14	CD458721
c 32	745.4	12.8	844	28	BZ574513
c 33	743.6	12.8	832	12	BG923768
34	741	12.7	741	14	CD279174
35	741	12.7	966	28	BZ575002
c 36	740.4	12.7	1089	9	AU081124
37	739.8	12.7	1003	28	BZ576686
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c 39	739.2	12.7	914	28	BZ569398
c 40	738.6	12.7	863	14	CF752100
41	733.8	12.6	950	28	BZ571129
42	733.2	12.6	811	29	ATH517156
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ALIGNMENTS

RESULT 1
AJ281552/c
LOCUS 1070 bp mRNA linear EST 30-JUN-2000
DEFINITION 4A3A-P6F11-F Anopheles gambiae immune competent 4A3A Anopheles gambiae cDNA clone 4A3A-P6F11, mRNA sequence.
ACCESSION AJ281552
VERSION AJ281552.1 GI:6929432
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
REFERENCE 1 (bases 1 to 1070)
AUTHORS Dimopoulos, G., Casavant, T.B., Chang, S., Scheetz, T., Roberts, C., Donohue, M., Schultz, J., Benes, V., Bork, P., Ansorge, W., Soares, M.B., and Kafatos, F.C.
TITLE Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
MEDLINE 20300950
PUBMED 10841561
COMMENT Contact: Dimopoulos G
Fotis C. Kafatos laboratory
European Molecular Biology Laboratory
Meyhofstrasse 1, 69117 Heidelberg, Germany.

CD458286 Fg08_09a0
BG838279 Gc01_10e0
CD459092 Fg08_08e0
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CD459085 Fg08_08d0
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		/note="Vector: p7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: EcoRI; Site 2: NotI; sequenced from forward priming site which reads from the 3' end of the cDNA. The 4A3A is a directionally cloned and normalized cDNA library that was constructed from the 4A3A cell line cDNA primed cDNA according to: Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."	
ORIGIN		18.1%; Score 1055.8; DB 9; Length 1070;	
Query Match		Best Local Similarity 99.7%; Pred. No. 2.1e-256; Indels 1; Gaps 1;	
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QY	4527	GTTCGCAAACTATTAACTGGCACTACTTACTCTAGCTTCCGGCAACAATTAATAGA	4586
DB	1070	GTTCGCAAACTATTAACTGGCACTACTTACTCTAGCTTCCGGCAACAATTAATAGA	1011
QY	4587	CTGGATGGAGGGGATAAAGTTTCAGGACCACTTCTCGCTCGGCTTCCGGCTGGCTG	4646
DB	1010	CTGGATGGAGGGGATAAAGTTTCAGGACCACTTCTCGCTCGGCTTCCGGCTGGCTG	952
QY	4647	GTTTATGCTGATAAATCTGGAGCCGCTGAGCGTGGCTCGCGGTATCATTCAGCACT	4706
DB	951	GTTTATGCTGATAAATCTGGAGCCGCTGAGCGTGGCTCGCGGTATCATTCAGCACT	892
QY	4707	GGGGCAGATGTTAAGCCCTCCGATCTAGTATCTACAGACGGGAGTCAGCAAC	4766
DB	891	GGGGCAGATGTTAAGCCCTCCGATCTAGTATCTACAGACGGGAGTCAGCAAC	832
QY	4767	TATGATGAACGAAATAGACAGATCGCTGAGATAGTGGCTCTACTGATTAAAGATTGTA	4826
DB	831	TATGATGACGAAATAGACAGATCGCTGAGATAGTGGCTCTACTGATTAAAGATTGTA	772
QY	4827	ACTGTACAGCAAGTTTACTCATATATCTTTAGTTAGTTAAACTTCAATTTTAAT	4886
DB	771	ACTGTACAGCAAGTTTACTCATATATCTTTAGTTAGTTAAACTTCAATTTTAAT	712
QY	4887	TAAAGGATCTAGTGAAGATCTTTTGTATAATCTCATGACCAAAATCCCTTAACGTGA	4946
DB	711	TAAAGGATCTAGTGAAGATCTTTTGTATAATCTCATGACCAAAATCCCTTAACGTGA	652
QY	4947	GTTTTCTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAGAGATCTTTGAGATCC	5006
DB	651	GTTTTCTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAGAGATCTTTGAGATCC	592
QY	5007	TTTTTTCTGGCGTATCTGCTGTGCAACAAAACACCCCGCTACAGCGGTGGT	5066
DB	591	TTTTTTCTGGCGTATCTGCTGTGCAACAAAACACCCCGCTACAGCGGTGGT	532
QY	5067	TTGTTTCCGGATCAAGAGTACCAACTCTTTTCCGAAGGTAACTGGCTTCAGCAGC	5126
DB	531	TTGTTTCCGGATCAAGAGTACCAACTCTTTTCCGAAGGTAACTGGCTTCAGCAGC	472
QY	5127	GCAGATACCAAACTCTGCTTCTAGTGGCGGTAGTGGCCACCACTTCAAGACTC	5186
DB	471	GCAGATACCAAACTCTGCTTCTAGTGGCGGTAGTGGCCACCACTTCAAGACTC	412
QY	5187	TGTAGCACCGCTACATACCTCGCTCTGTAATCTGTTACAGTGGCTGCTCCAGTGG	5246
DB	411	TGTAGCACCGCTACATACCTCGCTCTGTAATCTGTTACAGTGGCTGCTCCAGTGG	352
QY	5247	CGATAAGTCGTGTTCTTACCGGTTGGACTCAAGACGATAGTTACCGGATAGGCGCAGC	5306
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LOCUS		sequence.	
ACCESSION		BM438846	
VERSION		BM438846.1 GI:18460568	
KEYWORDS		EST.	
SOURCE		Ictalurus punctatus (channel catfish)	
ORGANISM		Ictalurus punctatus	
REFERENCE		Feng, J., Kucuktas, H., Kocabas, A., Li, P. and Liu, Z.	
AUTHORS		Transcriptome of channel catfish (Ictalurus punctatus): initial	
TITLE		analysis of expressed sequence tags from the liver	
JOURNAL		Unpublished (2002)	
COMMENT		Contact: Liu Z	
		The Fish Molecular Genetics and Biotechnology Laboratory,	
		Department of Fisheries and Allied Aquacultures and Program of Cell	
		and Molecular Biosciences	
		Auburn University	
		203 Swingle Hall, Auburn University, Auburn, AL 36849, USA	
		Tel: 334 844 4054	
		Fax: 334 844 9208	
		Email: zliu@acesag.auburn.edu	
		Seq primer: M13 Reverse.	
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Query Match		Best Local Similarity 99.5%; Pred. No. 8.6e-239;	
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DB	1	GCATTTTGCCTTCTGCTTTTGTCTACCCAGAGACGCTGGTGAAGTAAAGATGCTGAA	60
QY	4072	GATCAGTTGGGTGCACGAGTGGGTACATCGAACTGGATCTCAACAGCGGTAAGATCCTT	4131
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QY 4132 GAGAGTTTTCGCCCGAAGAAAGCTTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGT 4191
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QY 4192 GCGCGGTATATATCCGTTATTGACCGCGGGAAGAGCACTCGTTCGCGGCAATACACTAT 4251
Db 181 GCGCGGTATATATCCGTTATTGACCGCGGGAAGAGCACTCGTTCGCGGCAATACACTAT 240
QY 4252 TCTCAGATGACTTGGTTGGTACTCAGCAGTACAGAAAGAGCACTTTTAAAGTTCTGCTATGT 4311
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QY 4312 ACAGTAGAAGTAATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4371
Db 301 ACAGTAGAAGTAATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
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Db 420 CAATGTAACTCGCTTGCATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGA 479
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QY 4671 CGGTGAGCGTGGTCTCGCGGTATCATTTGAGCACTGGGCGCCAGATGGTAAGCCCTCCCG 4730
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QY 4791 CGCTGAGATGAGTGCCTCACTGATTAAGCAATGATGATGATGATGATGATGATGATGATG 4850
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RESULT 3
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LOCUS
DEFINITION
43A-P4G8-F Anopheles gambiae immune competent 4A3A Anopheles
gambiae cDNA clone 4A3A-P4G8, mRNA sequence.
ACCESSION
AJ281480
VERSION
AJ281480.1 GI:6929360
KEYWORDS
EST.
SOURCE
Anopheles gambiae (African malaria mosquito)
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

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REFERENCE
AUTHORS
Dimopoulos, G., Casavant, T.L., Chang, S., Scheetz, T., Roberts, C.,
Donohue, M., Schultz, J., Benes, V., Bork, P., Ansoorge, W., Soares, M.B.
and Kafatos, F.C.
TITLE
Anopheles gambiae pilot gene discovery project: identification of
mosquito innate immunity genes from expressed sequence tags
generated from immune-competent cell lines
Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
20300950
PUBMED
10841561
COMMENT
Contact: Dimopoulos G
Fotis C. Kafatos laboratory
European Molecular Biology Laboratory
Meyerohofstrasse 1, 69117 Heidelberg, Germany.
FEATURES
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forward priming site which reads from the 3' end of the
cDNA. The 4A3A is a directionally cloned and normalized
cDNA library that was constructed from the 4A3A cell line
oligo-T primed cDNA according to: Bonaldo, Lennon & Soares
(1996) : Normalization and Subtraction: Two approaches to
Facilitate Gene Discovery, Genome Research 6, 791-806."

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ORIGIN

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Query Match 15.9%; Score 924; DB 9; Length 1004;
Best Local Similarity 99.0%; Pred. No. 5.9e-223;
Matches 1001; Conservative 1; Mismatches 2; Indels 7; Gaps 7;
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QY 4796 AGATAGGTGCTCTACTGATTAAGCAATGCTACTCTCAGACCAAGTTTACTCATATATAC 4855
Db 830 AGATA-GTGCGCTCTACTGATTAAGCAATGCTACTCTCAGACCAAGTTTACTCATATATAC 772
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QY 4976 TAGAAAAGATCAAGAGTCTTCTGAGATCCTTTTCTGCGGCTAAATCTGCTGCTGCTG 5035
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.

1 (bases 1 to 1004)
Dimopoulos, G., Casavant, T.L., Chang, S., Scheetz, T., Roberts, C.,
Donohue, M., Schultz, J., Benes, V., Bork, P., Ansoorge, W., Soares, M.B.
and Kafatos, F.C.
Anopheles gambiae pilot gene discovery project: identification of
mosquito innate immunity genes from expressed sequence tags
generated from immune-competent cell lines
Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)

10841561

Contact: Dimopoulos G

Fotis C. Kafatos laboratory

European Molecular Biology Laboratory

Meyerohofstrasse 1, 69117 Heidelberg, Germany.

Location/Qualifiers

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/clone_lib="Anopheles gambiae immune competent 4A3A"

/notes="Vector: p773D-Pac (Pharmacia) with a modified

polylinker; Site 1: EcoRI; Site 2: NotI; sequenced from

forward priming site which reads from the 3' end of the

cDNA. The 4A3A is a directionally cloned and normalized

cDNA library that was constructed from the 4A3A cell line

oligo-T primed cDNA according to: Bonaldo, Lennon & Soares

(1996) : Normalization and Subtraction: Two approaches to

Facilitate Gene Discovery, Genome Research 6, 791-806."

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molecular weight, water-soluble components."

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ORIGIN

Query Match	15.7%	Score 916.2	DB 14	Length 973
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DB	24	ATTTAGTGGCACTTTTCGGGAAATGTCGGCGAAACCCCTATTGTTTATTTTCTAAA	83	
QY	3893	TACATTCAAAATATGATATCCGCTCATGAGACAATAAACCCCTGATTAATGCTTCAATAATATT	3952	
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DB	144	GAAAAAGGAGATGATGAGTATTCACCATTTCCGTGTCGCCCTTATTCCTTTTTCGGG	203	
QY	4013	CATTTTCCTTCCTGTTTTCCTTCACCCAGAAACGCTGGTGAAGTAAAGATGCTGAAG	4077	
DB	204	CATTTTCCTTCCTGTTTTCCTTCACCCAGAAACGCTGGTGAAGTAAAGATGCTGAAG	263	
QY	4073	ATCAGTTGGGTGCAGAGTGGTTTACATPCGAACCTGGATCTCAACAGCGGTAAAGTCCCTG	4133	
DB	264	ATCAGTTGGGTGCAGAGTGGTTTACATPCGAACCTGGATCTCAACAGCGGTAAAGTCCCTG	323	
QY	4133	AGAGTTTCGCCCGGAGAAAGCTTTTCCAATGATGAGCACATTTTAAAGTTCCTGCTATGTG	4193	
DB	324	AGAGTTTCGCCCGGAGAAAGCTTTTCCAATGATGAGCACATTTTAAAGTTCCTGCTATGTG	383	
QY	4193	CGCGGTATTAATCCCGTATTGACCGCGGCGAAGACAACTCGGTCCGCGCATACACTATT	4255	
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DB	504	CAGTAAGAGAAATATGCACTGCTGCCATAACCATGATGATAACTCTGGCGGCAACTTAC	563	
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DB	564	TTCTGACAAACGATCGGAGGACCGAAGAGCTTAACCGCTTTTGTGCAACATATGGGGGATC	6233	
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Db	923	TCGTAGTTATCTACACGAGGGGAGTCCAGGCAACTATGATGACGAAATAGA	973
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LOCUS	Fg08_09a03_R Fg08 AAFc ECORC Fusarium graminearum complex_substrate		
DEFINITION	Gibberella zeae cDNA clone Fg08_09a03, mRNA sequence.		
ACCESSION	CD458286		
VERSION	CD458286.1	GI:31373026	
KEYWORDS	EST.		
SOURCE	Gibberella zeae		
ORGANISM	Gibberella zeae		
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocerales; Nectriaceae; Gibberella.		
AUTHORS	Watson, R.J., Heys, R., Chapados, J., Couroux, P., Harris, L.J., Hattori, J., Lacroix, C., Ouellet, T., Robert, L.S., Singh, J.A., Sprott, D. and Tinker, N.A.		
TITLE	A cDNA library prepared from Fusarium graminearum grown on a complex plant substrate		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Watson, Robert.J. Eastern Cereal and Oilseed Research Centre Agriculture and Agri-Food Canada Bldg. 20, Central Experimental Farm, Ottawa, Ontario, K1A 0C6, CANADA Tel: (613) 759-1655 Fax: (613) 759-1701 Email: watsonrj@agr.gc.ca.		
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	ubstrate"		
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Query Match	15.2%; Score 885.6; DB 14; Length 917;		
Best Local Similarity	99.6%; Pred. No. 3.2e-213;		
Matches	888; Conservative 0; Mismatches 4; Indels 0; Gaps 0;		
QY	3833	ATACAGTGGCACTTTTCGGGAAATGTGCGGGAACCCCTATTTGTTTATTTCTAAA	3892
Db	26	ATTAGTGGCACTTTTCGGGAAATGTGCGGGAACCCCTATTTGTTTATTTCTAAA	85
QY	3893	TACATTCAAATATGTATCGCTCATGACACATAACCCCTGATAATGCTCAATATATT	3952
Db	86	TACATTCAAATATGTATCGCTCATGACACATAACCCCTGATAATGCTCAATATATT	145
QY	3953	GAAGAAGGAAGATGTAGTATTCAACATTTCCGTGTCGCCCTATTTCCCTTTTTCGGG	4012
Db	146	GAAGAAGGAAGATGTAGTATTCAACATTTCCGTGTCGCCCTATTTCCCTTTTTCGGG	205
QY	4013	CATTTTGCCTTCCTTTTGTCTACCCAGAACGCTGGTGAAGATGCTGAAG	4072
Db	206	CATTTTGCCTTCCTTTTGTCTACCCAGAACGCTGGTGAAGATGCTGAAG	265
QY	4073	ATCAGTGGGTGACAGTGGGTATCATCGAATGGAATCTCAACAGCGGTGAATCCTTG	4132
Db	266	ATCAGTGGGTGACAGTGGGTATCATCGAATGGAATCTCAACAGCGGTGAATCCTTG	325

/mol_type="mRNA"
/cultivar="1035"
/db_xref="taxon:45687"
/clone="Gc01.10e07"
/tissue_type="Leaves, stem"
/clone_lib="Gc01_AAFc_ECORC_cold_stressed_Glycine_clandestina"
/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI; Site 2: XhoI; Plants incubated at 2 degrees under 12 hours of light/day. Harvested after only 2-3 days of cold treatment. cDNA was prepared with the Uni-Zap cDNA kit from Stratagene. Eco RI adapters were linked followed by digest with Xho I/Eco RI and ligated to pBluescript."

ORIGIN

Query Match 15.0%; Score 873; DB 12; Length 935;
Best Local Similarity 97.9%; Pred. No. 5.1e-210;
Matches 878; Conservative 14; Mismatches 4; Indels 1; Gaps 1;

3833 ATACAGGTGGCACTTTTCGGGAAATGTGCGGGAACCCCTATTGTTTATTTTCTAAA 3892
Db |||||
32 ATTTAGGTGGCACTTTTCGGGAAATGTGCGGGAACCCCTATTGTTTATTTCTAAA 91
Qy |||||
3893 TACATTCAATATGATCGCTCATGAGACAATAACCCCTGATAAATGCTTCAATAATATT 3952
Db |||||
92 TACATTCAATATGATCGCTCATGAGACAATAACCCCTGATAAATGCTTCAATAATATT 151
Qy |||||
3953 GAAAAAGGAGAGATGAGTATTCACATTCGTTGTCGCCCTTATTCCTTTTTCGGG 4012
Db |||||
152 GAAAAAGGAGAGATGAGTATTCACATTCGTTGTCGCCCTTATTCCTTTTTCGGG 211
Qy |||||
4013 CATTTTGCCTTCTGTTTGTCTACCCAGAACGCTGTTGAAAGTAAAGATGCTGAAG 4072
Db |||||
212 CATTTTGCCTTCTGTTTGTCTACCCAGAACGCTGTTGAAAGTAAAGATGCTGAAG 271
Qy |||||
4073 ATCAGTTGGTGACGAGTGGGTTACATCGAATCGATCTCAACAGCGGTAAGATCCTTG 4132
Db |||||
272 ATCAGTTGGTGACGAGTGGGTTACATCGAATCGATCTCAACAGCGGTAAGATCCTTG 331
Qy |||||
4133 AGAGTTTTCGCCCCGGAAGAACGTTTTCGAATGAGAGCTTTTAAAGTTCGCTATG 4192
Db |||||
332 AGAGTTTTCGCCCCGGAAGAACGTTTTCGAATGAGAGCTTTTAAAGTTCGCTATG 391
Qy |||||
4193 GCGCGGTATATCCGTTATGACGCGGGAAGAGCAACTCGTGCAGCATACACTATT 4252
Db |||||
392 GCGCGGTATATCCGTTATGACGCGGGAAGAGCAACTCGTGCAGCATACACTATT 451
Qy |||||
4253 CTGAGATGACTTGTGTTGAGTACTCACAGTCTCAGAAAAAGCATCTTACGGATGGA 4312
Db |||||
452 CTGAGATGACTTGTGTTGAGTACTCACAGTCTCAGAAAAAGCATCTTACGGATGGA 511
Qy |||||
4313 CAGTAAGAGATATGATGAGTGTGCTGCTGATACATGATGATACACTGCGG-CCAACTTA 4371
Db |||||
512 CAGTAAGAGATATGATGAGTGTGCTGCTGATACATGATGATACACTGCGGCCCCAACTTA 571
Qy |||||
4372 CTTCTGACACAGATCGGAGACCGAAGGAGTAAACCGCTTTTTCGCAACATGGGGAT 4431
Db |||||
572 CTTCTGACACAGATCGGAGACCGAAGGAGTAAACCGCTTTTTCGCAACATGGGGAT 631
Qy |||||
4432 CATGTAATCGCTTGTATGTTGGGAACCGGAGCTGAATGAGCCATACCAACGAGAG 4491
Db |||||
632 CATGTAATCGCTTGTATGTTGGGAACCGGAGCTGAATGAGCCATACCAACGAGAG 691
Qy |||||
4492 CGTGACACAGATCGCTGATGAGTAAAGCAACAGTGTGCAACTTAACTTGGGAA 4551
Db |||||
692 CGTGACACAGATCGCTGATGAGTAAAGCAACAGTGTGCAACTTAACTTGGGAA 751
Qy |||||
4552 CTACTTACTAGCTTCCCGCAACAATTAATAGACTGATGAGGCGGATGAAAGTTGCA 4611
Db |||||
752 CTACTTACTAGCTTCCCGCAACAATTAATAGACTGATGAGGCGGATGAAAGTTGCA 811
Qy |||||
4612 GGACCACTTCTGCGCTCGGCCCTTCGGCTGGTGTATTTGCTGATAAATCTGGAGCC 4671
Db |||||

Db 812 GGACCACCTTCTGGCTCGGCCCTTCGGCTGGTGGKTTATTGCTGATAWATCTGGRGCC 871

Qy 4672 GGTGAGCGTGGTCTCGCGGTATCATTTGAGCATCGGGCGAGATGTAAGCCCTCC 4728

Db 872 GKGAGCGTGGKCTCGCGGTATCATTTGAGCATCGGGCGAGATGTAAGCCCTCC 928

RESULT 7

CD459092 918 bp mRNA linear EST 03-JUN-2003

LOCUS Fg08_08e02_R_Fg08_AAFc_ECORC_Fusarium_graminearum_complex_substrate

DEFINITION Gibberella_zeae cDNA clone Fg08_08e02, mRNA sequence.

ACCESSION CD459092

VERSION CD459092.1 GI:31373832

KEYWORDS EST.

SOURCE Gibberella zeae

ORGANISM Gibberella zeae

REFERENCE Watson,R.J., Heyes,R., Chapados,J., Couroux,P., Harris,L.J., Hattori,J., Lacroix,C., Ouellet,T., Robert,L.S., Singh,J.A., Sprott,D. and Tinker,N.A.

AUTHORS A cDNA library prepared from Fusarium graminearum grown on a complex plant substrate

TITLE Unpublished (2003)

JOURNAL Contact: Watson, Robert.J.

COMMENT Eastern Cereal and Oilseed Research Centre

Agriculture and Agri-food Canada

Bldg. 20, Central Experimental Farm, Ottawa, Ontario, K1A 0C6, CANADA

Tel: (613) 759-1655

Fax: (613) 759-1701

Email: watsonrj@agr.gc.ca.

FEATURES

1..918

Location/Qualifiers

/organism="Gibberella zeae"

/mol_type="mRNA"

/strain="DAOM 180378"

/db_xref="taxon:5518"

/clone="Fg08_08e02"

/tissue_type="Mycelium"

/dev_stage="Asexual"

/lab_host="E. coli DH10B"

/clone_lib="Fg08_AAFc_ECORC_Fusarium_graminearum_complex_substrate"

/note="Vector: pBluescript II+; Site 1: EcoRI; Site 2: XhoI; Fusarium graminearum grown on a complex plant substrate-- wheat leaves treated to remove most of the low molecular weight, water-soluble components."

ORIGIN

Query Match 14.9%; Score 865.4; DB 14; Length 918;
Best Local Similarity 99.2%; Pred. No. 4.4e-208;
Matches 888; Conservative 2; Mismatches 3; Indels 2; Gaps 2;

3833 ATACAGTGGCACTTTTCGGGAAATGTGCGGGAACCCCTATTGTTTATTTCTAAA 3892
Qy |||||
24 ATTTAGTGGCACTTTTCGGGAAATGTGCGGGAACCCCTATTGTTTATTTCTAAA 83
Db |||||
3893 TACATTTCAATATGATATCGCTCATGAGACAATAACCCCTGATAAATGCTTCAATAATATT 3952
Qy |||||
84 TACATTTCAATATGATATCGCTCATGAGACAATAACCCCTGATAAATGCTTCAATAATATT 143
Db |||||
3953 GAAAAAGGAGAGATGAGTATTCACATTTCCGTGTCGCCCTTATTCCTTTTTCGGG 4012
Qy |||||
144 GAAAAAGGAGAGATGAGTATTCACATTTCCGTGTCGCCCTTATTCCTTTTTCGGG 203
Db |||||
4013 CATTTTGCCTTCTGTTTGTCTACCCAGAACGCTGTTGAAAGTAAAGATGCTGAAG 4072
Qy |||||
204 CATTTTGCCTTCTGTTTGTCTACCCAGAGACGCTGTTGAAAGTAAAGATGCTGAAG 263
Db |||||
4073 ATCAGTTGGTGACAGTGGGTTACATCGAATGATCTCAACAGCGGTAAGATCCTTG 4132
Qy |||||

QY	4713 A 4713	CD459085	872 bp	mrna	linear	EST 03-JUN-2003	
Db	841 A 841	Fg08_08d03_R Fg08_AAF_CECORC Fusarium_graminearum_complex_substrate					
		Gibberella zeae cDNA clone Fg08_08d03, mRNA sequence.					
RESULT 9		CD459085	872 bp	mrna	linear	EST 03-JUN-2003	
LOCUS		Fg08_08d03_R Fg08_AAF_CECORC Fusarium_graminearum_complex_substrate					
DEFINITION		Gibberella zeae cDNA clone Fg08_08d03, mRNA sequence.					
ACCESSION		CD459085					
VERSION		CD459085.1	GI:31373825				
KEYWORDS		EST.					
ORGANISM		Gibberella zeae					
REFERENCE		Gibberella zeae					
AUTHORS		Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.					
TITLE		1 (bases 1 to 872)					
JOURNAL		Watson, R.J., Heyes, R., Chapados, J., Couroux, P., Harris, L.J., Hattori, J., Iacoiro, C., Ouellet, T., Robert, L.S., Singh, J.A., Sprott, D. and Tinker, N.A.					
COMMENT		A cDNA library prepared from Fusarium graminearum grown on a complex plant substrate					
FEATURES		Unpublished (2003)					
Source		Contact: Watson, Robert J.					
		Eastern Cereal and Oilseed Research Centre					
		Agriculture and Agri-food Canada					
		Bldg. 20, Central Experimental Farm, Ottawa, Ontario, K1A 0C6, CANADA					
		Tel: (613) 759-1655					
		Fax: (613) 759-1701					
		Email: watsonrj@agr.gc.ca					
		Location/Qualifiers					
		1..872					
		/organism="Gibberella zeae"					
		/mol_type="mrna"					
		/strain="DAOM 180378"					
		/db_xref="taxon:5518"					
		/clone="Fg08_08d03"					
		/tissue_type="mycelium"					
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		/lab_host="E. coli DH10B"					
		/clone_lib="Fg08_AAF_CECORC_Fusarium_graminearum_complex_substrate"					
		/note="Vector: pBluescript II+; Site_1: EcoRI; Site_2: XhoI; Fusarium graminearum grown on a complex plant substrate-- wheat leaves treated to remove most of the low molecular weight, water-soluble components."					
ORIGIN							
Query Match		14.3%	Score 832.8;	DB 14;	Length 872;		
Best Local Similarity		99.2%;	Pred. No. 8.1e-200;				
Matches 831;		Conservative 5;	Mismatches 2;	Indels 0;	Gaps 0;		
QY	3846	TTTTTCGGGAAATGTGCGGGAACCCCTATTGTTGTTATTTCTTAAATACATTCAATAT	3905				
Db	35	TTTTTCGGGAAATGTGCGGGAACCCCTATTGTTATTTTCTTAAATACATTCAATAT	94				
QY	3906	GTATCCGCTCATGAGACAATAACCTGATAAATGCTCAATAATATTGAAAAGGAAGAG	3965				
Db	95	GTATCCGCTCATGAGACAATAAACCCTGATAAATGCTCAATAATATTGAAAAGGAAGAG	154				
QY	3966	TATGAGTATTCACATTTCCGTGCGCCCTATTCCCTTTTTCGGGCAATTTGCTTCC	4025				
Db	155	TATGAGTATTCACATTTCCGTGCGCCCTATTCCCTTTTTCGGGCAATTTGCTTCC	214				
QY	4026	TGTTTTCTCACCAGAAAACGCTGGTGAAGTAAAGATCTGAAGATCAGTTGGGTGC	4085				
Db	215	TGTTTTCTCACCAGAGACGCTGGTGAAGTAAAGATCTGAAGATCAGTTGGGTGC	274				
QY	4086	ACGAGTGGTTACATCGAATCGATCTCAACAGCGGTAAAGTCTTGGAGTTTCGCC	4145				
Db	275	ACGAGTGGTTACATCGAATCGATCTCAACAGCGGTAAAGTCTTGGAGTTTCGCC	334				
QY	4146	CGAAGAACGTTTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGTGCGGGTATTATC	4205				
Db	335	CGAAGAACGTTTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGTGCGGGTATTATC	394				
QY	4206	CCGTATTGACGCGCGGCAAGAGCAACTCGGTGCGGCATACACTATTCTCAGAATGACTT	4265				
Db	395	CCGTATTGACGCGCGGCAAGAGCAACTCGGTGCGGCATACACTATTCTCAGAATGACTT	454				
QY	4266	GTTTGTAGTACTCACCAGTTCACAGAAAAGCATTTTACCGATGGCATGACAGTAAGAAT	4325				
Db	455	GTTTGTAGTACTCACCAGTTCACAGAAAAGCATTTTACCGATGGCATGACAGTAAGAAT	514				
QY	4326	ATGCAGTCTGCTCATACCATGATGATATAACTCTGGGCGCACTTACTTCTGACAACGAT	4385				
Db	515	ATGCAGTCTGCTCATACCATGATGATATAACTCTGGGCGCACTTACTTCTGACAACGAT	574				
QY	4386	CGGAGGACCGAAGAGCTAAACCGCTTTTTCGACAACTATGGGGATCATGTAACTCGCT	4445				
Db	575	CGGAGGACCGAAGAGCTAAACCGCTTTTTCGACAACTATGGGGATCATGTAACTCGCT	634				
QY	4446	TGATCTGTTGGGAACCGGAGCTGAATGAAGCCCATCAACAGCAGCGTGACACCAAGAT	4505				
Db	635	TGATCTGTTGGGAACCGGAGCTGAATGAAGCCCATCAACAGCAGCGTGACACCAAGAT	694				
QY	4506	GCCTGTAGCAATGGCAACAAACGTTGCGCAACTATTAACTGCGCACTACTTACTCTAGC	4565				
Db	695	GCCTGTAGCAATGGCAACAAACGTTGCGCAACTATTAACTGCGCACTACTTACTCTAGC	754				
QY	4566	TTCCCGGCAACAAATTAATAGACTGGATGGAGCGGATAAAGTTGCAAGCACTTCTGGG	4625				
Db	755	TTCCCGGCAACAAATTAATAGACTGGATGGAGCGGATAAAGTTGCAAGCACTTCTGGG	814				
QY	4626	CTCGGCCCTTCCGGCTGGCTGTTTATTGCTGATTAATCTGGAGCCGTTGAGCGTGGG	4683				
Db	815	CTCGGCCCTTCCGGCTGGCTGTTTATTGCTGATTAATCTGGAGCCGTTGAGCGTGGG	872				
RESULT 10		CF269652/c					
LOCUS		CF269652	1073 bp	mrna	linear	EST 13-AUG-2003	
DEFINITION		Fcycolid844 Fragilariopsis cylindrus SMART cDNA library (Clontech)					
		Fragilariopsis cylindrus cDNA clone Antarctic 5', mRNA sequence.					
ACCESSION		CF269652					
VERSION		CF269652.1	GI:33631539				
KEYWORDS		EST.					
SOURCE		Fragilariopsis cylindrus					
ORGANISM		Fragilariopsis cylindrus					
REFERENCE		1 (bases 1 to 1073)					
AUTHORS		Mock, T. and Valentin, K.					
TITLE		EST analysis of freezing tolerance in the Antarctic diatom					
JOURNAL		Fragilariopsis cylindrus: Detection of numerous cold adaptation					
COMMENT		related genes and gene transfer events					
		Unpublished (2003)					
		Contact: Mock T					
		Biological Oceanography					
		Alfred-Wegener-Institute for Polar and Marine Research					
		Am Handelshafen 12, D-27570 Bremerhaven, Germany					
		Tel: +49 471 4831 1893					
		Fax: +49 471 4831 1425					
		Email: tmock@awi-bremerhaven.de					
		sequence with unknown function					
		PCR Primers					
		BACKWARD: 5'lambdaTriplex2					
		FORWARD: 3'lambdaTriplex2					
		Seq primer: ctcgggaagcgccattgtgtgtt					
FEATURES		Location/Qualifiers					
source		1..1073					
		/organism="Fragilariopsis cylindrus"					
		/mol_type="mrna"					
		/strain="Antarctic"					

/db_xref="taxon:186039"
/clone="Antarctic"
/clone_lib="Fragilariopsis cylindrus SMART cDNA library
(Clontech)"
/note="vector: pTriplex2; total polyA was used for
first-strand synthesis with SMART IV oligos and CDS
III/3/PCR primer. Double strand cDNA synthesis was done by
LD PCR using the following program: 95°C for 5 min
denaturation and subsequent 20 cycles at 95°C (2min) and
68°C (6min). After SfiI digestion the cDNA was
fractionated with CHROMA Spin-400 columns. These cDNAs
were ligated overnight into pTriplex2 vectors."

ORIGIN

Query Match 14.2%; Score 825; DB 14; Length 1073;
Best Local Similarity 96.5%; Pred. No. 8.1e-198;
Matches 884; Conservative 0; Mismatches 25; Indels 7; Gaps 4;

QY 4914 TGATAATCTCATGACCAAAATCCCTTAACGTTGAGTTTTCGTTCCACTGAGCGTCAGACCC 4973
DB 964 TTATTGTCTCATGCCAAATCCCTTAACGTTGAGTTTTCGTTCCACTGAGCGTCAGACCC 905
QY 4974 CGTAGAAAAGATCAAGAGATCTCTTCAGATCTCTTTTCTGCGGTAACTCTGCTGTT 5033
DB 904 CGTAGAAAAGATCAAGAGATCTCTTCAGATCTCTTTTCTGCGGTAACTCTGCTGTT 845
QY 5034 GCAACAAAAAACCACCGCTTACAGCGGTGTTTGTTCGCGATCAAGAGCTACCAAC 5093
DB 844 GCAACAAAAAACCACCGCTTACAGCGGTGTTTGTTCGCGATCAAGAGCTACCAAC 785
QY 5094 TCTTTTCCGAGTAACT--GGCTTCAGCAGAGCGC-AGATACCAAAATAC-TGTCTT 5148
DB 784 TCTTTTCCGAGTAACTGGCTTCNAGCAGAGCGCNAGATACCAAAATACNTGTCTT 725
QY 5149 CTAGTGTAGCG--TAGTTAGGCACACACTTAAGAACTCTGTAGACCGCCTACAPAC 5206
DB 724 CTAGTGTAGCNGTAGTTANGGCGCCACTTCAAGAACTCTGTAGCACCCTACATACC 665
QY 5207 TCCTCTGCTAATCTTGTACCAAGTGTCTGCTGCGAGTGGGATAGTCTGTCTTACCG 5266
DB 664 TCCTCTGCTAATCTTGTACCAAGTGTCTGCTGCGAGTGGGATAGTCTGTCTTACCG 605
QY 5267 GGTGGACTCAAGACGATGTTACCGGATAAGCGCAGCGGTGCGGTGAAACGGGGGTT 5326
DB 604 GGTGGACTCAAGACGATGTTACCGGATAAGCGCAGCGGTGCGGTGAAACGGGGGTT 545
QY 5327 CGTGACACAGCCCGCTTGAGCGGACGACCTACACCGAACTGAGATACCTACAGCGT 5386
DB 544 CGTGACACAGCCCGCTTGAGCGGACGACCTACACCGAACTGAGATACCTACAGCGT 485
QY 5387 AGCTATGAGAAAGCGCCAGCTTCCCGAAGGAGAAAGCGGACAGTATCCGTAACG 5446
DB 484 AGCTATGAGAAAGCGCCAGCTTCCCGAAGGAGAAAGCGGACAGTATCCGTAACG 425
QY 5447 GCAGGTTCGGAACAGAGAGCGCACAGGGAGCTTCCAGGGGAAACGGCTGTATCTTT 5506
DB 424 GCAGGTTCGGAACAGAGAGCGCACAGGGAGCTTCCAGGGGAAACGGCTGTATCTTT 365
QY 5507 ATAGTCTCGGTTTCGCCACCTTGACTGAGCGTCAATTTTGTGATGCTGCTAG 5566
DB 364 ATAGTCTCGGTTTCGCCACCTTGACTGAGCGTCAATTTTGTGATGCTGCTAG 305
QY 5567 GGGGGCGAGCCTATGAAAAAGCGCAGCAACCGGCTTTTACGGTTCTTGGCTTTT 5626
DB 304 GGGGGCGAGCCTATGAAAAAGCGCAGCAACCGGCTTTTACGGTTCTTGGCTTTT 245
QY 5627 GTGGCCTTTTCTCATGTTCTTTCCTGCGTTATCCCTGATCTGTGGATAACCGTA 5686
DB 244 GCTGGCCTTTTCTCATGTTCTTTCCTGCGTTATCCCTGATCTGTGGATAACCGTA 185
QY 5687 TTACGCCCTTTGAGTGAGTGATGATACCGCTCGCGCAGCGCAACGACCGAGCGAGT 5746
DB 184 TTACGCCCTTTGAGTGAGTGATGATACCGCTCGCGCAGCGCAACGAGCGAGT 125

QY 5747 CAGTAGCGAGGAGCGGAGAGCGCCCAATACGCAACCGCCTCTCCCGCGCTTGGC 5806
DB 124 CAGTAGCGAGGAGCGGAGAGCGCCCAATACGCAACCGCCTCTCTCCCGCGCTTGGC 65
QY 5807 CGATTCTAATGCGAG 5822
DB 64 CGATTCTAATGCGAG 49

RESULT 11
BM438950
LOCUS
DEFINITION Iplvr00491 Liver cDNA library Ictalurus punctatus cDNA 5', mRNA
ACCESSION BM438950
VERSION BM438950.1 GI:18460672
KEYWORDS EST.
SOURCE Ictalurus punctatus (channel catfish)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
Ictaluridae; Ictalurus.
1 (bases 1 to 854)
Feng,J., Kucuktas,H., Kocabas,A., Li,P. and Liu,Z.
Transcriptome of channel catfish (Ictalurus punctatus): initial
analysis of expressed sequence tags from the liver
Unpublished (2002)
Contact: Liu ZJ
The Fish Molecular Genetics and Biotechnology Laboratory,
Department of Fisheries and Allied Aquacultures and Program of Cell
and Molecular Biosciences
Auburn University
203 Swingle Hall, Auburn University, Auburn, AL 36849, USA
Tel: 334 844 4054
Fax: 334 844 9208
Email: zliu@acesag.auburn.edu
Seq primer: M13 Reverse.
Location/Qualifiers
1..854
/organism="Ictalurus punctatus"
/mol_type="mRNA"
/db_xref="taxon:7998"
/clone_lib="Liver cDNA library"
/note="Organ: Liver; Vector: pSport1; Site_1: NotI;
Site_2: SalI"

ORIGIN

Query Match 14.2%; Score 824.6; DB 12; Length 854;
Best Local Similarity 99.3%; Pred. No. 9.7e-198;
Matches 849; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 4012 GCATTTTGCTTCTCTGTTTGTCTACCCAGAAACGCTGGTGAAGTAAAGTGTGAA 4071
DB 1 GCATTTTGCTTCTCTGTTTGTCTACCCAGATACGCTGGTGAAGTAAAGTGTGAA 60
QY 4072 GATCAGTTGGGTGACAGTGGG-TTACATCGAACTGGATCTCAACAGCGTAAGATCTT 4130
DB 61 GATCAGTTGGGTGACAGTGGGTTACATCGAATGATCTCAACAGCGTAAGATCTT 120
QY 4131 TGAGAGTTTCCCGCGGAAGACGTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATG 4190
DB 121 TGAGAGTTTCCCGCGGAAGACGTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATG 180
QY 4191 TGGCGCGTATTATCCCGTATTGACCGGGCAAGCAACTCGGTCCGCGCATACACTA 4250
DB 181 TGGCGCGTATTATCCCGTATTGACCGGGCAAGCAACTCGGTCCGCGCATACACTA 240
QY 4251 TTCTCAGAAATGACTTGGTTGAGTACTCACCAGTACAGAAAAGCACTTTACGGATGGCAT 4310
DB 241 TTCTCAGAAATGACTTGGTTGAGTACTCACCAGTACAGAAAAGCACTTTACGGATGGCAT 300
QY 4311 GACAGTAAGAGAAATTATGCAAGTGTGTGTCATAACCATGAGTGATACACTGCGCGCAACTT 4370

301 GACAGTAAGAGAAATATGACGTGCTGCCATCAACATGATGATTAACACTGCGCCAACTT 360
4371 ACTTCTGACAAACGATCGAGGACCGAAGAGCTAACCGCTTTTGTGCAACATGGGGGA 4430
361 ACTTCTGACAAACGATCGAGGACCGAA-GAGCTAACCGCTTTTGTGCAACATGGGGGA 419
4431 TCATGTAACCTGCCCTTGATCGTTGGGAACCGAGCTGAATGAAGCCATACCAACGACGA 4490
420 TCATGTAACCTGCCCTTGATCGTTGGGAACCGAGCTGAATGAAGCCATACCAACGACGA 479
4491 GCGTGACACACGATGCTGTAGCAATGCGCAACACGCTTGGCCAACTATTAACTGGCGA 4550
480 GCGTGACACACGATGCTGTAGCAATGCGCAACACGCTTGGCCAACTATTAACTGGCGA 539
4551 ACTACTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGGGGATTAAGTTGC 4610
540 ACTACTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGGGGATTAAGTTGC 599
4611 AGGACCACTTCTGCGCTCGGCCCTTCCGCTCGCTGGCTTTATTGCTGATAATCTGGAGC 4670
600 AGGACCACTTCTGCGCTCGGCCCTTCCGCTCGCTGGCTTTATTGCTGATAATCTGGAGC 659
4671 CGGTGAGCGTGGCTCTCGCGGTATCAATTCAGCAGCTGGGGCCAGATGGTAAAGCCCTCCG 4730
660 CGGTGAGCGTGGCTCTCGCGGTATCAATTCAGCAGCTGGGGCCAGATGGTAAAGCCCTCCG 719
4731 TATCGTAGTATPCTACAGACGGGAGTCAGGCACTATGATGAACGAAATAGACAGAT 4790
720 TATCGTAGTATPCTACAGACGGGAGTCAGGCACTATGATGAACGAAATAGACAGAT 779
4791 CGGTGAGTGGCTCTACTGATTAAGCAATGGTAACCTGTCAGACCAAGTTTACTCATA 4850
780 CGGTGAGTGGCTCTACTGATTAAGCAATGGTAACCTGTCAGACCAAGTTTACTCATA 839
4851 TATACTTTAGATTGA 4865
840 TATGCTTGAGATTGA 854

RESULT 12
CD458333
LOCUS
DEFINITION
Fg08_09e07_R Fg08_AAFRC_EOORC_Fusarium_graminearum_complex_substrate
Gibberella zeae cDNA clone Fg08_09e07, mRNA sequence.
ACCESSION
CD458333
VERSION
CD458333.1 GI:31373073
KEYWORDS
EST.
SOURCE
Gibberella zeae
ORGANISM
Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE
1 (bases 1 to 870)
Watson,R.J., Heys,R., Chapados,J., Couroux,P., Harris,L.J.,
Hattori,J., Lacroix,C., Ouellet,T., Robert,L.S., Singh,J.A.,
Sprott,D. and Tinker,N.A.
A cDNA library prepared from Fusarium graminearum grown on a
complex plant substrate
JOURNAL
Unpublished (2003)
COMMENT
Contact: Watson, Robert.J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-Food Canada
Bldg. 20, Central Experimental Farm, Ottawa, Ontario, K1A 0C6,
CANADA
Tel: (613) 759-1655
Fax: (613) 759-1701
Email: watsonrj@agr.gc.ca.
Location/Qualifiers
1..870
/organism="Gibberella zeae"
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XhoI; Fusarium graminearum grown on a complex plant
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molecular weight, water-soluble components."

ORIGIN

Query Match 14.1%; Score 819.6; DB 14; Length 870;
Best Local Similarity 99.2%; Pred. No. 1.8e-196;
Matches 841; Conservative 3; Mismatches 2; Indels 2; Gaps 2;
3833 ATACAGGTGGACATTTTCGGGGAATGTGCGGGAACCCCTATTGTTTATTTCTAAA 3892
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3893 TACATTCAAAATATGATCCGCTCATGAGACAATAAACCTGTATAATGCTTCAATAATT 3952
84 TACATTCAAAATATGATCCGCTCATGAGACAATAAACCTGTATAATGCTTCAATAATT 143
3953 GAAAAAGGAAGATGATGATTTCAACATTTCCGTTGCGCCCTTATTCCTTTTTCGCG 4012
144 GAAAAAGGAAGATGATGATTTCAACATTTCCGTTGCGCCCTTATTCCTTTTTCGCG 203
4013 CATTTTGCCTTCTCTTTTGTCTCAACCCAGAACGCTGGTGAAGTAAAGATGCTGAAG 4072
204 CATTTTGCCTTCTCTTTTGTCTCAACCCAGAACGCTGGTGAAGTAAAGATGCTGAAG 263
4073 ATCAGTTGGGTGCACGAGTGGTTATCATCGAATCTGATCTCAACAGCGGTAAGATCTTG 4132
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4133 AGAGTTTTCGCCCCGAGAACGTTTTCGAATGATGACACTTTTAAAGTTCTGCTATGTG 4192
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4193 GCGCGTATATCCCGTATTGACCGCGGCAAGAGCAACTCGGTCGCCGCATACACTATT 4252
384 GCGCGTATATATCCCGTATTGACCGCGGCAAGAGCAACTCGGTCGCCGCATACACTATT 443
4253 CTCAGAAATGACTTGGTTGATGATCTACAGTCTACAGAAAGCATCTTACGGATGGATGA 4312
444 CTCAGAAATGACTTGGTTGATGATCTACAGTCTACAGAAAGCATCTTACGGATGGATGA 503
4313 CAGTAAGAGAAATATGACGTGCTGCCATTAACCATGATGATTAACACTGCGGCCAATTC 4372
504 CAGTAAGAGAAATATGACGTGCTGCCATTAACCATGATGATTAACACTGCGGCCAATTC 563
4373 -TTCTGACAAACGATCGAGGACCGAAGAGCTAACCGCTTTTGTGCAACATGGGGGAT 4431
564 TTTCTGACAAACGATCGAGGACCGAA-GAGCTAACCGCTTTTGTGCAACATGGGGGAT 622
4432 CATGTAACCTGCCCTTGATCGTTGGGAACCGAGCTGAATGAAGCCATACCAACGACGAG 4491
623 CATGTAACCTGCCCTTGATCGTTGGGAACCGAGCTGAATGAAGCCATACCAACGACGAG 682
4492 CGTGACACCAACGATGCTGTAGCAATGCGCAACACGCTTGGCCAACTATTAACTGGCGAA 4551
683 CGTGACACCAACGATGCTGTAGCAATGCGCAACACGCTTGGCCAACTATTAACTGGCGAA 742
4552 CTACTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGGGGATTAAGTTGCA 4611
743 CTACTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGGGGATTAAGTTGCA 802
4612 GGACCACTTCTGCGCTCGGCCCTTCCGCTGGCTGTTTATTCGTGATAATCTGAGGCC 4671
803 GGACCACTTCTGCGCTCGGCCCTTCCGCTGGCTGTTTATTCGTGATAATCTGAGGCC 862
4672 GGTGAGCG 4679

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Db      863  GKGAGCG 870

RESULT 13
BZ572284/c
LOCUS   BZ572284
DEFINITION msh2_2572.x3 msh Pseudomonas aeruginosa genomic clone msh2_2572,
GENOMIC SURVEY SEQUENCE.
ACCESSION BZ572284
VERSION   BZ572284.1 GI:27207345
KEYWORDS  GSS.
SOURCE    Pseudomonas aeruginosa
ORGANISM  Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 1249)
Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
Burns,J.L., Kaul,R. and Olsen,M.V.
Whole-Genome-Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.
Location/Qualifiers
1..1249
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library."
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Best Local Similarity 93.0%; Pred. No. 2e-195;
Matches 952; Conservative 0; Mismatches 61; Indels 11; Gaps 9;

QY      4799  TAGTGCCCTCAGTAAAGATGTTGTAAGTGTGACAGCAAGTTTACTCATATATCTTT 4858
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QY      4979  AAAAGATCAAGGATCTTCTTGAGATCTTTTCTGCGGATCTGCGGATCTGCTGCTGCAA 5038
Db      941  GAAAGACCAAGATCTTCTGAGAACCTTTTTCGTGCGGTAAT-TGCTGCTGC-AA 884
QY      5039  CAAAAAACCCCGCTTACAGCGGTGGTGTGTTGTCGGGATCAAGAGCTACCACTCTTT 5098
Db      883  CAAAAAACCCCGCTTACAGCGGTGGTGTGTTGTCGGGATCAAGAGCTA-CAACTCTTT 827
QY      5099  TTCCGAAGTAACTGGCTTACAGAGCGCAGATACCAATACTGTCCTTCTAGTGTAGC 5158
Db      826  TTCGAGAGGTANCT-GCTTCAGAGCGCAGATACCAATACTGTCCTTCTAGTGTAGC 768
QY      5159  CTTAGTTAGGCCACCACTTCAAGACTCTGTAGACCGCCTACATCTGCTCTGTGATA 5218
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library."
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Query Match 14.0%; Score 815.6; DB 28; Length 1249;
Best Local Similarity 93.0%; Pred. No. 2e-195;
Matches 952; Conservative 0; Mismatches 61; Indels 11; Gaps 9;

QY      4799  TAGTGCCCTCAGTAAAGATGTTGTAAGTGTGACAGCAAGTTTACTCATATATCTTT 4858
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QY      4919  ATCTCATGACCAAACTCCCTTAAGTGAATTTTCCTCACTGAGCGTCAGACCCCGTAG 4978
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QY      5039  CAAAAAACCCCGCTTACAGCGGTGGTGTGTTGTCGGGATCAAGAGCTACCACTCTTT 5098
Db      883  CAAAAAACCCCGCTTACAGCGGTGGTGTGTTGTCGGGATCAAGAGCTA-CAACTCTTT 827
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Db      826  TTCGAGAGGTANCT-GCTTCAGAGCGCAGATACCAATACTGTCCTTCTAGTGTAGC 768
QY      5159  CTTAGTTAGGCCACCACTTCAAGACTCTGTAGACCGCCTACATCTGCTCTGTGATA 5218
Db      767  GGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATCTGCTCTGTGATA 708

QY      5219  TCCTTTACCAAGTGGCTGCTGCCAGTGGCGATAAGTCTGTCTTACCGGTTGGACTCAA 5278
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Db      467  CAGGAGAGCGGACGAGGAGCTTCCAGGGGAAACCGCTGATATCTTTATAGTCTGTGCG 408
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Db      407  GGTTCGCGCACTCTGACTTGAAGCGTGAATTTTGTGATGCTGCTCAGGGGGGCGAGCC 348
QY      5579  TATGGAAGGACGCGAGCAACCGGCGCTTTTACGGTTCTCTGGCCTTTTGTGGCCTTTTG 5638
Db      347  TATGGAAGGACGCGAGCAACCGGCGCTTTTACGGTTCTCTGGCCTTTTGTGGCCTTTTG 288
QY      5639  CTCACATGTTCTTCTGCGCTTATCCCTGATTCCTGATCTGTGATTAACCGCTTTTAC 5698
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QY      5699  AGTGAGCTGATACCGTTCGCGCAGCGCAAGCGGACCGGACGCGAGTCAAGTGAAGCAG 5758
Db      227  AGTGAGCTGATACCGTTCGCGCAGCGCAAGCGGACCGGACGCGAGTCAAGTGAAGCAG 168
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Db      167  AAGCGAAGAGCGCCCAATAACGCAACCGCTCTCCCGCGCGCTTGGCCGATTCATTAA 108
QY      5819  GCAG 5822
Db      107  GCAG 104

RESULT 14
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LOCUS   BZ577702
DEFINITION msh2_5533.y2 msh Pseudomonas aeruginosa genomic clone msh2_5533,
GENOMIC SURVEY SEQUENCE.
ACCESSION BZ577702
VERSION   BZ577702.1 GI:27212763
KEYWORDS  GSS.
SOURCE    Pseudomonas aeruginosa
ORGANISM  Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 1126)
Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
Burns,J.L., Kaul,R. and Olsen,M.V.
Whole-Genome-Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.
Location/Qualifiers

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Best Local Similarity 90.4%; Pred. No. 4e-195;
Matches 938; Conservative 0; Mismatches 91; Indels 9; Gaps 6;

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QY 3941 TTCAATATATGAAAAGGAGATGATGATTTCAACATTTCCGTGTCGCCCTTATTC 4000
DB TTTCAATATATGAAAAGGAGATGATGATTTCAACATTTCCGTGTCGCCCTTATTC 212

QY 4001 CTTTTTTGCGCATTTTGCCTTCTCTTTTCTCACCAGAAACGCTGGTGAAGTAA 4060
DB CTTTTTTGCGCATTTTGCCTTCTCTTTTCTCACCAGAAACGCTGGTGAAGTAA 272

QY 4061 AAGATGCTGAAGATCATGTTGGTGACGAGTGGTTACATCAATGGATCTCAACAGC 4120
DB AAGATGCTGAAGATCATGTTGGTGACGAGTGGTTACATCAATGGATCTCAACAGC 332

QY 4121 GTAAGATCTTTGAGATTTTCCGCCGGAAGACGTTTTTCCAAATGATGACATTTTAAAG 4180
DB GTAAGATCTTTGAGATTTTCCGCCGGAAGACGTTTTTCCAAATGATGACATTTTAAAG 392

QY 4181 TTCTGCTATGTGCGCGGTATTTATCCGTTATTTGACCGCGGCAAGAGCAACTCGGTGCGC 4240
DB TTCTGCTATGTGCGCGGTATTTATCCGTTATTTGACCGCGGCAAGAGCAACTCGGTGCGC 452

QY 4241 GCATACATTTCTCAGATGATCTGGTTGAGTACTACCACTGACAGAAAGCATCTTA 4300
DB GCATACATTTCTCAGATGATCTGGTTGAGTACTACCACTGACAGAAAGCATCTTA 512

QY 4301 CGGATGCGCATGACAGTAAGAGATTTATGACGCTGCTGCTAATACCATGATGATAACTG 4360
DB CGGATGCGCATGACAGTAAGAGATTTATGACGCTGCTGCTAATACCATGATGATAACTG 572

QY 4361 CGGCCAACTTACTTCTGACAAACGATCGGAGGACGAGGAGCTAACCGCTTTTTCGACA 4420
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DB ACATGGGGATCATGTAATCTGCGCTTGATCGTTGGGAACCGAGCTGAATGAGCCATAC 692

QY 4481 CAAACGACGCGGTGACACACGATGCTGTAGCAATGGCAACACGCTGCGCAAACTAT 4540
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QY 4601 AT-AAAAGTTGAGACACATCTTCTGCGCTCGGCCCTTCCGCTGGCTGGTTATTGCTGAT 4659
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QY 4660 AAATCTGAGCGGTGACGCTGGCTCTCGCGGTATCAATGACGACTCGGGCCAGATGGT 4719
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Db 933 AAACCTTCCGATCGGAATTTTCTACCGACCGGGAGTCAGGAACTATTGTTTAAAC 992

QY 4778 GAAATAGACAGATCGCTGAGAT-AGTGCCTCAGTATTAGCACTTGGTAACTGCACAC 4836

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QY 4897 TAGGTGAAGATCCTTTT 4914

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DEFINITION 5', mRNA sequence.
ACCESSION CD649375
VERSION CD649375.1 GI:31906346
KEYWORDS EST.
SOURCE Crassostrea virginica (eastern oyster)
ORGANISM Crassostrea virginica
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
Ostreidae; Ostreidae; Crassostrea.
REFERENCE 1 (bases 1 to 819)
AUTHORS Peatman,E., Kucuktas,H., Li,P., He,C., Feng,J., Wei,X. and Liu,Z.
TITLE Differentially expressed oyster (Crassostrea virginica) genes after exposure to mercury
JOURNAL Unpublished (2003)
COMMENT Contact: Liu Z
The Fish Molecular Genetics and Biotechnology Laboratory,
Department of Fisheries and Allied Aquacultures and Program of Cell
and Molecular Biosciences
Auburn University
203 Swingle Hall, Auburn University, Auburn, AL 36849, USA
Tel: 334 844 4054
Fax: 334 844 9208
Email: zliu@acesag.auburn.edu
Seq primer: M13 Reverse.
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ORIGIN

Query Match 13.9%; Score 808; DB 14; Length 819;
Best Local Similarity 99.9%; Pred. No. 1.6e-193;
Matches 819; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 4132 GAGAGTTTTCGCCCGGAGAAACGTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGT 4191

Db 121 GAGAGTTTTCGCCCGGAGAAACGTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGT 180

QY 4192 GGCGCGGTATTATCCCGTATTGACCGGGCAAGCAACTCGGTTCGCCGATACACTAT 4251

Db 181 GGCGCGGTATTATCCCGTATTGACCGGGCAAGCAACTCGGTTCGCCGATACACTAT 240

QY 4252 TCTCAGATGACTGTTGTTGACTACTCACCAGTCAAGAAAAGCATCTTACGGATGGCATG 4311


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Db      301  ACAGTAAGAGAAATTATGCAGTCTGCCATACCACTAGTATACACTGCGGCCAACTTA 360
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Job time : 8922 secs

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